GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 30, 2003, 09:49:41; Search time 22 Seconds (without alignments) 64.100 Million cell updates/sec Run on:

SEQ1 183 1 mcsnlstcvlgklsqelhklqtyprtntgsgtpg 34 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01263		oncorhy		oncorhy		P01258 homo sapien		cani						-		-		P19824 chlamydomon		Q8xjd8 clostridium		esche		schiz		schizosa	P32795 saccharomyc	P40856 saccharomyc	Ŋ	P03869 agrobacteri	. Q46920 escherichia	P18752 xenopus lae	
SUMMARIES	ΩI		CAL_ANGJA	CAL2_ONCKE	CAL_CHICK	CAL3_ONCKI	CALO_RAT	CALO_HUMAN	CALO_MOUSE	CAL_CANFA	CAL_SHEEP	KPPR_SPIOL	KPPR_MESCR	CAL_BOVIN	CAL_PIG	KPPR_ARATH	KPPR_WHEAT	NO2B_SOYBN	SP2P_BACSU	KPPR_CHLRE	A2AP_MOUSE	EX7L_CLOPE	YB98_HUMAN	EAE_ECO27	TRIO_HUMAN	RE15_SCHPO	NUOB_BUCAI	NG79_SCHPO	YME1_YEAST	S185_YEAST	YHD0_YEAST	IPT_AGRT4	YQCD_ECOLI	ZO72_XENLA	
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QQ2574 saccharomyc Q9rOhO mus musculu PO7872 rattus norv Q99kg7 mus musculu Q64430 mus musculu PO705 rattus norv P29539 saccharomyc Q9z810 chlamydia p Q42363 brachydanio P37101 syrachocyst Q15991 eisenia foe P76134 escherichia
MEC3_YEAST CAO1_MOUSE CAO1_RAT CAO1_RAT MPS4_MOUSE AT7A_MOUSE AT7A_RAT RIF1_YEAST RIF1_YEAST RY54_CHUEN APA1_BRARE RPPR_SYMY3 KLOW_ELSFO YDEM_ECOLI
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474 661 661 671 1492 1916 1916 332 331 385
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ALIGNMENTS

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CAL2_ONCKE
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Lucpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99315214; PubMed-10387083; Hashimoto Y., Toma K., Nishikido J., Yamamoto K., Haneda K., Inazu T., Valentine K.G., Opella S.J.; Effects of glycosylation on the structure and dynamics of eel calcitonin in micelles and lipid bilayers determined by nuclear
                                             PHARMACEUTICAL: Available under the names Calcimar (Rhone-Poulenc Rorer), Miacalcin (Novartis) or Forcaltonin (Unigene). Used for the treatment of Paget's disease and hypercalcemia in malignancy. SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (G-115 PROVIDE AMIDE GROUP)
Biochemistry 30:10444-10450(1991).
-!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            magnetic resonance spectroscopy";
Biochemistry 38:8377-8384(1999).
-1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
                                                                                                                                                                                                                                        HSSP; P01262; IBMC.
INTERPROJ 1PR001693; Calcitconin-like.
InterPro; IPR001935; Calcitconin_A.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITCONINA.
SMART; SM00113; CALCITCONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
Cleavage on pair of basic residues; Amidation; Hormone; Signal;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178; DB 1; Length 13st Pred. No. 1.1e-18; Oreman O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      15179 MW; BDD8867AE113B2A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 AA
                                                                                                                                                                                                                                                                                                                                                                     CALCITONIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Noda T., Narita K.; "Amino acid sequence of eel calcitonin."; J. Biochem. 79:353-359(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   97.3%; Scor
100.0%; Pre
                                      THOSE IONS IN THE BONES.
                                                                                                                                                                                                      EMBL, Y00765, CAA68734.1; -. PIR, A01530, TCON.
PIR, A31229, A31229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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114
89
114
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136 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR.
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                                                                                                                                                                                                                                                                                                                                             Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcitonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAL_ANGJA
P01262;
                                                                                                                                                                                                                                                                                                                                                                            DISULFID
MOD_RES
SEQUENCE
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Fotts J.T., Lequin R.M., Habener J.F., Singer F.R., Niall H.D., Potts J.T. Jr., Cequin R.M., Habener J.F., Singer F.R., Niall H.D., "Chemistry and physiology of the calcitonins: some recent advances."; (In) Taylor S. (eds.); Endocrinology 1971: proceedings of the third international symposium, pp. 316-323, Heinemann Medical Books, London (1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus keta (Chum salmon), and Oncorhynchus nerka (Sockeye salmon), and Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon). Bukaryota: Metazota; Chordata: Craniata: Vertebrata; Euteleostomi; Actinopterygii: Neopterygii; Teleostei; Euteleostei; Protacanthopterygii: Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pless J., Bauer W., Bossert H., Zehnder K., Guttmann S.;
"Synthesis of two natural salmon calcitonins.";
Nature New Biol. 240:62-631972).
--i- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                           Length 32;
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                                                                                                                                                                                                                                                                                                                AMIDATÍON.
AFC93549F8048922 CRC64;
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                -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
PIR; A01529; TCBE.
PDB; 1BKU; 18-MAR-99
INTERPRO; IPR001693; Calcitonin-like.
InterPro; IPR001935; Calcitonin_A.
FRAM; PF00214; Calc_GRP_IAPP; 1.
PRNINTS; PR00270; CALCITONINA.
SMART; SM00113; CALCITONINA, 1.
PROSITE; PS00258; CALCITONIN, 1.
PROSITE; PS00258; CALCITONIN, 1.
PLOMORE, Amidation; 3D-structure.
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF THOSE IONS IN THE BONES.
-!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
PIR; A01531; TCON2.
PIR; A01531; TCON2.
PIR; D01531; TCON2.
IN 1001531; TCON2.
PIR; D01502; TEWU.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin-like.
Pfam; PF00214; Calc. CGRP. IAPP; I.
PRINTS; PR00270; CALCITONINA.
                                                                                                                                                                                                                                                                                                                                                                                           Score 159; DB 1;
Pred. No. 1.3e-16;
2; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSNLSTCVLGKLSQELHKLQTYPRTDVGAGTP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=73047885; PubMed=4508400;
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PROSITE; PS00258; CALCITONIN; 1.
OF THOSE IONS IN THE BONES
                                                                                                                                                                                                                                                                                                             32 32
32 AA; 3418 MW;
                                                                                                                                                                                                                                                                                                                                                                                           .86.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.6
es 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAL2_ONCKE
P01264;
                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF THOSE IONS IN THE BONES.
-!- ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE CALCITONIN RELATED PEPTIDE PRECURSOR ARE OBTAINED BY TISSUE-SPECIFIC SPLICING
                                                                                                                                                                                                                                                                                          Calcitonin precursor.
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evidence for the expression of a lower vertebrate calcitonin-like gene in man and rat."; EMBO J. 4:2603-2607(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homma T., Watanabe M., Hirose, Kanai A., Kangawa K., Matsuo H., "Isolation and determination of the amino acid sequence of chicken calcitonin I from chicken ultimobranchial glands.";
J. Biochem. 100:459-467(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 71-117 FROM N.A.
MEDLINE=85102042; PubMed=3838160;
Lasmoles F., Jullienne A., Desplan C., Milhaud G., Moukhtar M.S.;
"Structure of chicken calcitonin predicted by partial nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
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Minvielle S., Cressent M., Delehaye M.C., Segond N., Milhaud
Jullienne A., Moukhtar M.S., Lasmoles F.;
"Sequence and expression of the chicken calcitonin gene.";
FEBS Lett. 223:63-68(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 12-138 FROM N.A.
MEDLINE=86030240; PubMed=4054101;
Lasmoles F., Jullienne A., Day F., Minvielle S., Milhaud G.,
Moukhtar M.S.;
                                  Indels
. No. 2.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                                   01-APR-1988 (Rel. 07, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                      AA.
                                  3; Mismatches
                                                                     2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP
                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X06312; -; NOT_ANNOTATED_CDS.
EMBL; X06313; -; NOT_ANNOTATED_CDS.
EMEL; X03012; CAA26796.1; -.
EMBL; M27563; AAA48648.1; -.
PIR; S00153; TCCH.
               Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of its precursor.";
FEBS Lett. 180:113-116(1985).
             87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X06311; CAA29630.1; -.
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                                  28; Conservative
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE SAME GENE
             Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                    CAL_CHICK
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                                                                                                                                                                 RESULT 4
CAL_CHICK
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Endocrinology 1971: proceedings of the third international symposium,
pp.316-323, Heinemann Medical Books, London (1972).
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF THOSE IONS IN THE BONES.
-!- MISCELLANEOUS: CALCITONIN 1 IS LESS ACTIVE THAN CALCITONINS 1 OR 2. ONLY THIS SPECIES OF SALMON POSSESSES CALCITONIN 3.
                                                                         PROSITE; PS00258; CALCITONIN; 1.
Cleavage on pair of basic residues; Amidation; Alternative splicing;
                                                                                                                                                                                AMIDATION (G-114 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY SEQUENCE.
Keutmann H.T., Lequin R.M., Habener J.F., Singer F.R., Niall H.D.,
Potts J.T. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pless J., Bauer W., Bossert H., Zehnder K., Guttmann S.; "Synthesis of two natural salmon calcitonins."; Nature New Biol. 240:62-63(1972).

-:- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncochynchus kisutch (Coho salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8019;
                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                  Length 138
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                             D -> E (IN REF. 2).
730B618CF724F248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
B57A3D9AF807E7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
PIR; B01531; TCON3.
HSSP: P01262; HBN.
InterPro; IPR001693; Calcitonin-like.
                                                                                                                                                                                                                                  Score 157; DB 1; L
Pred. No. 1.2e-15;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                     2 CSNLSTCVLGKLSQELHKLQTYPRINTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 32 AA.
                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                           CALCITONIN.
                                                                                                                   POTENTIAL.
        Interpro: IPR001693; Calcitonin-like.
Interpro: IPR00195; Calcitonin_A.
Pfam. PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=73047885; PubMed=4508400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN;
Hormone; Amidation.
                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                   85.8%;
84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3419 MW;
                                                                                                             25
79
113
138
88
113
56
                                                                                                                                                                                                                                               L Similarity 84.8
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
32 AA;
                                                                                                                                                                                                            AA;
                                                                                                                           26
82
118
82
113
56
138 f
                                                                                                    Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                CAL3_ONCKI P01265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
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                                                                                                                                                                 DISULFID
MOD_RES
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                  Query Match
                                                                                                                                          PEPTIDE
                                                                                                                                                                                                                                                  Best Local
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                                                                                                                   SIGNAL
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CAL3_ONCKI
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Dp
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Gaps

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Length 32; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-76210265; PubMed=1278175;

MEDLINE-76210265; PubMed=1278175;

Raulals D., Hagaman J., Ontjes D.A., Lundblad R.L., Kingdon H.S.;

The complete aniho-acid sequence of rat thyrocalcitonin.";

Eur. J. Blochem. 64:607-611(1976).

-! FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
OF THOSE IONS IN THE BONES.
-! SUBCELLULAR LOCATION: Secreted.
-! ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE CALCITONIN
RELATED PEPTIDE PRECURSOR ARE OBTAINED BY TISSUE-SPECIFIC SPLICING
                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81225842; PubMed-6264603;
Jacobs J.W., Goodman R.H., Chin W.W., Dee P.C., Habener J.F.,
Bell N.H., Potts J.T. Jr.;
"Calcitonin messenger RNA encodes multiple polypeptides in a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 83-136 FROM N.A. MEDLINE-81054790; PubMed=6933496; Amara S.G., David D.N., Rosenfeld M.G., Roos B.A., Evans R.M.; "Characterization of rat calcitonin mRNA."; Proc. Natl. Acad. Sci. U.S.A. 77:4444-4448(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenfeld M.G., Amara S.G., Evans R.M.;
"Alternative RNA processing events as a critical developmental regulatory strategy in neuroendocrine gene expression.";
Blochem. Soc. Symp. 49:27-44(1984).
       Score 154; DB 1; L
Pred. No. 6.7e-16;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF THE SAME GENE. SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                          2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                 AA.
                                                                                                                                                                                                136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87025913; PubMed-6400492;
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       84.2%;
84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V01230; CAA24540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA24538.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 213:457-459(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA24539.1;
                                          Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                 Calcitonin precursor.
Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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V01229;
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L00110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
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                                                                                                                                                              RESULT 6
                                                                                                                                                                            CALO_RAT
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-89386053; Pubmed=2571128;
Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;
"Structure and methylation of the human calcitonin/alpha-CGRP gene.";
Nucleic Acids Res. 17:6999-7011(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE).
AMIDATION (G-117 PROVIDE AMIDE GROUP).
A197358A802222F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALO_HUMAN STANDARD; PRT; 141 AA.
901256; 013937;
21-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
2015-tin precursor [Contains: Calcitonin, Ratacalcin (Calcitonin carboxyl-terminal peptide) (CCP) (PDN-21)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-86164952; PubMed-3485540;
MILLOY J.H., Edbrooke M.R., Craig R.K.;
"Ectopic synthesis of high-Mr calcitonin by the BEN lung carcinoma cell line reflects aberrant proteolytic processing.";
FEBS Lett. 198:71-79(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-SE166259, PubMed=3872459;
Johas V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,
Mermod J.-J., Evans R.M., Rosenfeld M.G.;
Malternative RNA processing events in human calcitonin/calcitonin
gene-related peptide gene expression.
Proc. Natl. Acad. sci. U.S.A. 82:1994-1998(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                HSSP, P01262, 1BKG.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001935; Calcitonin_A.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
SMART; SM00113; CALCITONIN, 1.
Cleavage on pair of basic residues; Signal; Amidation; Hormone; Glycoprotein; Alternative splicing.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1; Leus.
1.4e-08; Indels
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MEDLINE-84132556; PubMed=6546550;
le Moullec J.M., Jullienne A., Chenais J., Lasmoles Guliana J.M., Milhaud G., Moukhtar M.S.;
"The complete sequence of human preprocalcitonin.";
FEBS Lett. 167:93-97(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                            CALCITONIN
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MEDLINE=87213363; PubMed=3034287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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82
116
136
91
87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserv
PIR; A01525; TCRT
                                                                                                                                                                                                                                                                                                26
85
121
85
87
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                            PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                   PROPEP
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Fri May 30 10:10:23 2003

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                                                                                                                                        TISSUE=Thyroid carcinoms,
MEDLINE-92105127; PubMed-1701559;
Minvielle S., Giscard-Dartevelle S., Cohen R., Taboulet J., Labye F.,
Minvielle S., Giscard-Dartevelle S., Cohen R., Lasmoles F.,
"A novel calcitonin carboxyl-terminal peptide produced in medullary
thyroid carcinoma by alternative RNA processing of the
calcitonin gene-related peptide gene.";
J. Biol. Chem. 266:24627-24631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Katacalcin: a new plasma calcium-lowering hormone.";
Lancet 1:864-848(1983).
-i-FUNCTION: CALCITONIN CAUSES A RAPID BUT SHORT-LIVED DROP IN THE
LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE
LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE
LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE
INCORPORATION OF THOSE INNS IN THE BONES.
-i-FUNCTION: Katacalcin is a potent plasma calcium-lowering peptide.
-i-SUBCELLULAR LOCATION: Secreted.
-i-ATTERNATIVE PRODUCTS: 3 ISOFORMS. I (SHOWN HERE), 2 AND 3 (AC
PO6681); ARE PRODUCTS BY ALTERNATIVE SPLICING.
-i-SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                 Al-Kazwini S.J., Holman J.J., Marshall I.; "Expression and function of the human calcitonin/alpha-CGRP gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-85022523; Pubmed-6148938;
Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,
Baylin S.B.;
                                                                                                                                                                                                                                                                                                                                                                   Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D., Pettengill O.S., Craig R.K.; "Expression of the human calcitonin/CGRP gene in lung and thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure and expression of a gene encoding human calcitonin and calcitonin gene related peptide."; Biochem. Biophys. Res. Commun. 123:648-655(1984).
Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Foord S.M.,
Al-Kazwini S.J., Holman J.J., Marshall I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83166029; PubMed=6132180;
Hillyard C.J., Myers C., Abeyasekera G., Stevvensvenson J.C.,
Craig R.K., MacIntyre I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 85-116.
MEDIINE-72162720; PUDMed-5760861;
Weber R., Riniker B., Rittel W., Zuber H.;
"Human caloitonin. Structure of calcitonin M and D.";
Helv. Chim. Acta 51:1900-1905(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRÜCTURE BY NMR OF CALCITONIN.
MEDLINE-91159414; PubMed-2001366;
MOUTA A., Temussi P.A., Wunsch E., Bovermann G.;
"A 1H NMR study of human calcitonin in solution.";
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 49-141 FROM N.A. (ISOFORM 1).
                                                                              Biochem. Soc. Symp. 52:91-105(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X15943; CAA34070.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85230541; PubMed=2408883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 30:2364-2371(1991).
                                                                                                                         (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF KATACALCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 48-83 FROM N.A. MEDLINE=85022523; PubMed=61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X00356; CAA25103.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 4:715-724(1985).
                                                          health and disease.";
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinoma
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K03513; AAA52124.1; -. M12666; AAA51913.1; -. M12664; AAA51913.1; JOINED. M12665; AAA51913.1; JOINED.

EMBL; EMBL; EMBL;

EMBL;

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                                                                                                                                                                                                                                               Cleavage on pair of basic residues; Amidation; Alternative splicing; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                 AMIDATION (G-117 PROVIDE AMIDE GROUP). VSMPQNAN -> NHCPEESL (IN ISOFORM 2). M -> I (IN REF. 3). 99622305DD8B286F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-THYROID;

REDLINE-96400274; PubMed-8806650;
Rehli M., Luger K., Beier W., Falk W.;

Molecular cloning and expression of mouse procalcitonin.";

Blochem. Blophys. Res. Commun. 226:420-425(1996).

-! FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION OF THOSE IONS IN THE BONES.

-! SUBCELLULAR LOCATION: Secreted.

-! ALTERNATIVE PRODUCTS: 2 isoforms; I (shown here) and 2 (AC Q99JA0); are produced by alternative splicing.

-! SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 1;
Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                      KATACALCIN
                                                                                                                                                         InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001935; Calcitonin_A.
                                                                                                                                                                                    Pfam; PF00214; Calc_CGRP_IAPP; I.
SWRINTS; PR00270; CALCITONINA; I.
SMARY; SM00113; CALCITONIN; I.
PROSITE; PS00258; CALCITONIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                              92 N
15467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%;
51.5%;
L; X03662; CAA27299.1; -
L; M64486; AAA58403.1; -
L; M26095; AAA35501.1; -
A22716; TCHU.
; C22949; C22949.
                                                                    PIR; S07238; S07238.
PIR; S07242; S07242.
PIR; S07643; S07643.
HSSP, P01262; 1BKU.
Genew; HGNC:1437; CALCA.
MIM; 114130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                            25
82
116
141
91
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcitonin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                               141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         26
85
121
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALCA OR CALC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALO_MOUSE
P70160;
                                                                                                                                                                                                                                                                                                                                    DISULFID
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                        PROPEP
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                             SIGNAL
                            EMBL;
PIR; A
PIR; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Hormone;
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WITITE SO
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MEDLINE-92100867; PubMed-1758974;
MEDLINE-92100867; PubMed-1758974;
Medl J.A., Kwant M.M., Arnold I.C.J., Hazewinkel H.A.W.;
"Elucidation of the sequence of canine (pro)-calcitonin. A molecular biological and protein chemical approach.";
Regull. Pept. 35:189-195(1991).
-i- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: SYNTHESIZED BY C-CELLS OF THE THYROID GLAND.
                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (PROBABLE).
AMIDATION (G-117 PROVIDE AMIDE GROUP).
B7FIDD27F7E10DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                SMART; SM00113; CALCITONIN; 1. PROSTRIS; PS00208; CALCITONIN; 1. Cleavage on pair of basic residues; Signal; Amidation; Hormone; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             54.6%; Score 100; DB 1; Length 136; 51.5%; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-25, AND SEQUENCE OF 26-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                              CALCITONIN
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A60063; A60063.

HSSP: P01262; 1BKU.
INTEPPO; IPR001693; Calcitonin-like.
INTEPPO; IPR001935; Calcitonin_A.
PRINTS; PR00270; CALCITONINA.
SMART; SM00113; CALCITONIN; 1.
                                                       MGD; MGI:215123; Calca.
MGD; MGI:215123; Calca.
InterPro; IPR00169; Calcitonin-like.
InterPro; IPR00193; Calcitonin_A.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X56994; CAA40311.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcitonin precursor (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00258; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THOSE IONS IN THE BONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                116 A
15141 MW;
                   EMBL; x97991; CAA66630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                                                                                                                                                                                         25
82
116
136
91
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAL_CANFA
P41547;
                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                          PROPEP
PEPTIDE
                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
CAL_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cumaraswamy A., Borges M., Tamir H., Nelkin B.D.;
Lioning of a cDNA encoding sheep calcitonin from a thyroid C-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: CAUSES À RAPÍD BUT SHORT-LIVED DROP IN THE LEVEL OF CALCULM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION OF THOSE IONS IN THE BONES.
-i- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                               BY SIMILARITY.
AMIDATION (G-79 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00258; CALCITONIN; 1.
Cleavage on pair of basic residues; Amidation; Hormone; Signal.
                                                                                                                                                                                                                                                      ;;
0
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                                                                                                                                                                                                      Length 92;
                                                                                                                                                                                                                                                      11; Indels
Cleavage on pair of basic residues.
                                                                                                                                                            53B103230864039D CRC64;
                                                                                                                                                                                                         Score 90; DB 1;
Pred. No. 3.8e-06;
                                                                                                                 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                              2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                        CAL_SHEEP STANDARD; PRT; 143 AA. P01261; 21-JUL-1986 (Rel. 01, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Calcitonin precursor.
                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCITONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001935; Calcitonin_A.
Pfam. PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M98053; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Thyroid;
MEDLINE-93246256; PubMed-8482543;
                                                                                                                                      92
9974 MW;
                                                                                                                                                                                                         49.2%;
51.5%;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia, Eutheria, Ceta
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 126:269-273(1993).
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84
1118
143
93
  Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
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                                                                                                                                                                                                                         Local Similarity
nes 17; Conserv
                                                                                                                                                         92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                            25
47
78
                       NON_CONS
PEPTIDE
DISULFID
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MOD_RES
                                                                                                                                    NON_TER
SEQUENCE
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Query Match
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                       Roesler K.R., Ogren W.L.; "Nucleotide sequence of spinach cDNA encoding phosphoribulokinase."; Nucleic Acids Res. 16:7192-7192(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribulose 1,5-bisphosphate.
-!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
                                                                                                                                                                                                                                                      Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllidae, Caryophyllales, Chenopodiaceae, Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porter M.A., Milanez S., Stringer C.D., Hartman F.C.; "Purification and characterization of ribulose-5-phosphate kinase from spinach.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porter M.A., Hartman F.C.; "Commonality of catalytic and regulatory sites of spinach phosphoribulokinase: characterization of a tryptic peptide that contains an essential cysteinyl residue."; Biochemistry 25:7314-7318(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88087076; PubMed=2826432;
Porter M.A., Stringer C.D., Hartman F.C.;
"Characterization of the regulatory thioredoxin site of phosphoribulokinase.";
J. Biol. Chem. 263:123-129(1988).
-!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 7-402 FROM N.A.
MEDLINE-88329728; Pubmed-2843430;
Milanez S., Mural R.J.;
"Cloning and sequencing of CDNA encoding the mature form of phosphoribulokinase from spinach.";
                             Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: Calvin cycle.
-i- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
                                                     Indels
                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
(Phosphopentokinase) (PRRASE) (PRK)
 15658 MW; D4CEB15C5C06B663 CRC64;
               Score 72; DB 1; Len
Pred. No. 0.0024;
                                                                                         3; Mismatches
                                                                                                                                                                   402 AA
                                                                           2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. 245:14-23(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE BOND, AND PARTIAL SEQUENCE.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=88303351; PubMed=2841650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86129440; PubMed=3004354;
                          39.3%;
45.5%;
                                                   Conservative
                                                                                                                                                                   STANDARD;
             Query Match
Best Local Similarity
...^hes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 66:55-63(1988).
 143 AA;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 52-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 52-69.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3562;
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SEQUENCE
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-!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                        PRINTS; PR00478; PHRIBLKINASE.
PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
ATP-binding; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0478; PHRIBLKINASE.
PROSTIE; 9800567; PHOSPHORIBULOKINASE; 1.
Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
ATP-binding; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michalowski C.B., Derocher E.J., Bohnert H.J., Salvucci M.E., Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
(Phosphopentokinase) (PRKASE) (PRK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                              45007 MW; 450759B96A675C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORIBULOKINASE.
BY SIMILARITY.
88DC418E211EC975 CRC64;
                                                                                                                                                                                                                                                                                                                                             PHOSPHORIBULOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesembryanthemum crystallinum (Common ice plant)
                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2%; Score 68; DB 1; 44.8%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 SNLSTKFYGEVTQQMLKHQNFPGSNNGTG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SNLSTCVLGKLSQELHKLQTYPRTNTGSG 31
                                                                                                                                                                                                                                                                                                                  CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; X07654; CAA30499.1; -.
EMBL; M21338; AAA34036.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8,
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InterPro; IPR001324; PRK.
Pfam: PF00485; PRK; 1,
                                                                                                                                                       InterPro; IPR001324; PRK.
Pfam; PF00485; PRK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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106
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                                                                                                 PIR; JA0064; JA0064.
PIR; S02099; S02099.
                                                      PIR; A25182; A25182
                                                                                                                                                                                                                                                                                                                                                                                           402 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3est Local Similarity
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SEQUENCE
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Length 397;

DB 1;

Score 67;

36.68;

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MOD_RES
SEQUENCE
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A Brewer H.B. Jr., Ronan R.;
A Brewer H.B. Jr., Ronan R.;
Froco. Natl. Acad. Sci. U.S.A. 63:940-947(1969).
C -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION OF THOSE IONS IN THE BELONES TO THE CALCITONIN FAMILY.
R PIR: A01528; TCBO.
R InterPro; IPR001693; Calcitonin-like.
R InterPro; IPR001935; Calcitonin-like.
R PRINTS; PR00214; Calc. CGRP_IAPP; 1.
R PRINTS; PR002170; CALCITONINA.
R SMARY; SW00113; CALCITONIN; 1.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
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Potts J.T. Jr., Niall H.D., Keutmann H.T., Brewer H.B. Jr.
Deftos L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62; DB 1; Length 32;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                      Indels
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Proc. Natl. Acad. Sci. U.S.A. 59:1321-1328(1968).
[2]
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                      8;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSNLSTCVLSAYWKDLNNYHRFSGMGFGPETP 32
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    Pred. No. 0.038; Mismatches
                                                                                 3 SNLSTCVLGKLSQELHKLQTYPRTNTGSG 31
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40.68;
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44.8%;
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Best Local Similarity
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    Best Local Similarity
Matches 13; Conserv
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SEQUENCE
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P01259;
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MEDLINE-21016719; PubMed-11130712;
Theologis A., Ecker J. R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehher E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Greasy T.H., Dewar K.,
Dunn P., Ergu P., Feldblyum T.V. Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Johnkon Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 21, Last annotation update)
Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
(Phosphopentokinase) (PRRASE) (PRK).
AT1032006 OR T12021.4.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Neher R., Riniker B., Zuber H., Rittel W., Kahnt F.W.;
"Thyrocalcitonin. II. Structure of alpha-thyrocalcitonin.";
Helv. Chim. Acta 51:917-924(1968).
--i- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 61; DB 1; Length 32; 40.6%; Pred. No. 0.018; tive 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDE755ED2FE6EA09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF THOSE IONS IN THE BONES.
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InterPro; IPR001693; Calcitonin-11ke.
InterPro; IPR001935; Calcitonin_A.
Pfam; PF00214; Calc_GRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
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MEDLINE=91329732; PubMed=1651130;
MEDLINE=70161016; PubMed=5462122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00113; CALCITONIN; 1. PROSITE; PS00258; CALCITONIN; 1.
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Matches 13; Conservative
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P25697;
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                                                                                                                                                                 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I., Baid G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL; ACOTATO, CARTILLO II.

EMEL; ACOTATO, CARTILLO II.

PIR; S16583; S16583.

SWISS-SDRAGE; PES697; ARATH.

INTEPPO; IPRO01324; PRK.

PRINTS; PRO0478; PHINELKINASE.

PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.

Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle; ATP-binding; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 61; DB 1; Length 395; 41.4%; Pred. No. 0.29; Live 8; Mismatches 9; Indels

    -!- PATHWAY: Calvin cycle.
    -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.

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BY SIMILARITY.
4660A92EF7E39BC6 CRC64;
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                                                                                                                                                       thaliana.";
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Search completed: May 30, 2003, 09:50:56 Job time : 24 secs

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OM protein - protein search, using sw model

Run on:

May 30, 2003, 09:51:24 ; Search time 18 Seconds (without alignments) 191.200 Million cell updates/sec

Title: Perfect score:

SEQ1 183 1 mcsnlstcvlgklsqelhklqtyprtntgsgtpg 34 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

383519 Total number of hits satisfying chosen parameters:

383519 seqs, 101223694 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

(1) //GGID_6/PLOCATE_A//PLUDBAR_USO8_NEW_PUB.ppp:*
2. //GGID_6/PLOCATE_A//PUDBAR_USO8_NEW_PUB.ppp:*
3. //GGID_6/PLOCATE_A//PUDBAR_NESO.NEW_PUB.ppp:*
4. //GGID_6/PLOCATE_A//PUDBAR_USO6_PUBCOMB.ppp:*
5. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
6. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
7. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
8. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
9. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
9. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:*
9. //GGID_6/PLOCATE_A//PUDBAR_USO8_PUBCOMB.ppp:* /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US10_PuBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 15, Appl	Sequence 16, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 20, Appl	Sequence 10, Appl	Seguence 21, Appl	٦.	Sequence 12, Appl	Sequence 17, Appl			24,				Sequence 23, Appl	Sequence 19, Appl	Sequence 22, Appl
	DB ID	10 US-09-847-712-15	10 US-09-847-712-16	10 US-09-847-712-17	10 US-09-847-712-18	9 US-09-852-870A-20	10 US-09-847-712-10	9 US-09-852-870A-21	9 US-10-131-543-17	10 US-09-847-712-12	9 US-09-852-870A-17	9 US-10-131-543-26	9 US-10-131-543-25	9 US-10-131-543-24	9 US-09-852-870A-16	9 US-10-131-543-12	9 US-10-131-543-20	9 US-10-131-543-23	9 US-10-131-543-19	9 US-10-131-543-22
æ	Query Match Length DB	94.0 32	94.0 32	94.0 32	94.0 32	88.5 32	86.9 32	86.3 32	83.1 34	82.5 32	81.4 32	80.9 35	80.6 34	80.3 35	79.2 32	78.7 31	74.9 35	74.9 35	74.6 34	74.6 34
	Score	172	172	172	172	162	159	158	152	151	149	148	147.5	147	145	144	137	137	136.5	136.5
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18, 18, 18, 18, 18, 18, 18, 18, 18, 18,	Sequence 22, Appl Sequence 3, Appli Sequence 11, Appl Sequence 13820, A
24.64.64.64.64.64.64.64.64.64.64.64.64.64	10 US-09-813-345-22 ·10 US-09-746-945-3 10 US-09-847-712-11 10 US-09-815-242-13820
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136.5 136.1 131 131 123.5 102 100 100 100 100 100 100 100 100 100	74 60 56 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; salmon CT; LOCATION: (32)...(32); OTHER INFORMATION: An Fc domain attached at the C-terminus US-09-847-712-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - salmon CT
         Sequence 15, Application US/09847712
Fatent No. US20020090646A1
GENERAL IMPORMATION:
APPLICANT: LIU, CHUAN-FA
APPLICANT: MARSHALL, WILLIAM S.
APPLICANT: MARSHALL, WILLIAM S.
TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
FILE REFERENCE: A-684
CURRENT APPLICATION NUMBER: US/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,511
PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
94.0%; Score 172; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Preferred embodiments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09847712; Patent No. US2002009646A1
GENERAL INFORMATION: APPLICANT: LIU, CHUNN-FA
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 26
SOFWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 32
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US-09-847-712-15
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OTHER INFORMATION: Preferred embodiments - salmon CT
NAME/KEY: misc_feature
COCATION: (1)..(1)
OTHER INFORMATION: Fo domain attached at the C-terminus
NAME/KEY: misc_feature
LOCATION: (32)..(32)
OTHER INFORMATION: Position 32 is linked to an identical peptide sequence through
OTHER INFORMATION: optional linker
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. OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and third Ser
US-09-852-8708-20
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Pred. No. 3.2e-17;
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Patent No. US20020165132A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Goodman, Murray
APPLICANT: Goodman, Enthhonin Bridged Proteins
FITLE OF INVENTION: Lanthhonin Bridged Proteins
FILE OF INVENTION: Lanthhonin Bridged Proteins
FILE OF INVENTION: Lanthhonin Bridged Proteins
FILE OF INVENTION: 201-2-D
CURRENT APPLICATION NUMBER: US/09/852,870A
FRIOR APPLICATION NUMBER: US 09/384,601
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 20
LENGTH: 32
                                                  TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES FILE REFERENCE: A-684
CURRENT APPLICATION NUMBER: US/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,511
PRIOR PLING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 162; DB 9
Pred. No. 8e-16;
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               MARSHALL, WILLIAM S.
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APPLICANT: LIU, CHUAN-FA
APPLICANT: MARSHALL, WILLIAM S.
                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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96.9%;
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Best Local Similarity 96.9
Matches 31; Conservative
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Best Local Similarity
Matches 32; Conserva
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                                                                                                                                                                                                                              SEQ ID NO 18
LENGTH: 32
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NAME/KEY: misc_feature
LOCATION: (32)...(32)...(32)
OTHER INFORMATION: Position 32 is linked to an identical peptide sequence through an OTHER INFORMATION: optional linker
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APPLICANT: LIU, CHUN-FA
APPLICANT: MILLIAM S.
APPLICANT: MILLIAM S.
APPLICANT: REYNOLDS, ANGELA
ITTLE OF INVENTION: CALCITONIN-RELATED MOLECULES
FILE REPERENCE: A.684
CURRENT APPLICATION NUMBER: US/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN NOS: 26
SOFTWARE: PATENTIN VETSION 3.1
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100.0%; Pred. No. 3.2e-17;
Live 0; Mismatches 0;
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                  APPLICANT: REYNOLDS, ANGELA
TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
FILE REPERBACE: A-684
CURRENT APPLICATION NUMBER: US/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,511
PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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Patent No. US20020090646A1
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Patent No. US20020090646A1
GENERAL INFORMATION:
    MARSHALL, WILLIAM S.
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 26
SOFWARE: Patentin version 3.1
SEQ ID NO 3.2
LENCTH: 32
                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
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Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 32; Conserv
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US-09-847-712-17
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APPLICANT:
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FastSEQ for Windows Version 4.0
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84.4%;
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96.88;
                                                             TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 84.4
Matches 27; Conservative
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OTHER INFORMATION: Xaa
                                                                                                                                                             NAME/KEY: ACETYLATION
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Matches 30; Conserv
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US-10-131-543-17
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SOFTWARE: Fa
SEQ ID NO 17
LENGTH: 34
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Sequence 17, Application US/2003007270941

GENERAL INFORMATION:

APPLICANT: Cyr, John E.

APPLICANT: Pearson, Daniel A.

TITLE OF INVENTION: STABLILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC THIOFTHERS

FILE REFERENCE: 09744-016001

CURRENT FILING DATE: 2002-04-24

PRIOR PILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and second Ser US-09-852-870A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Osapay, George,
TITLE OF INVENTION: Lanchionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
PRIOR PAPLICATION NUMBER: US 09/384,601
PRIOR APPLICATION NUMBER: US 09/384,601
NUMBER OF SEQ ID NOS: 24
SCFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 32
                                                                                                                                                                                                                                                                                                    Score 159; DB 10;
Pred. No. 2.1e-15;
2; Mismatches 1;
              TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES FILE REFERENCE: A-684
CURRENT APPLICATION NUMBER: 02/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,511
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VOETSION 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09852870A Patent No. US20020165132A1 GENERAL INFORMATION:
APPLICANT: Goodman, Murray APPLICANT: Osapay, George
                                                                                                                                                                                                                                                                                                    86.9%;
90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
  REYNOLDS, ANGELA
                                                                                                                                                                                                                                                                                                    Query Match 86.9
Best Local Similarity 90.6
Matches 29; Conservative
                                                                                                                                                                                                                                       ; ORGANISM: eel
US-09-847-712-10
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                                                                                                                                                                                                                        TYPE: PRT
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: MARSHALL, WILLIAM S.
APPLICANT: REYNOLDS, ANGELA
TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
FILE REFERENCE: A-684
CURRENT APPLICATION NUMBER: US/09/847,712
CURRENT FILING DATE: 2001-05-02
PRIOR PPLICATION NUMBER: 60/201,511
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                Score 152; DB 9; I
Pred. No. 2.1e-14;
0; Mismatches 1;
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Pred. No. 2.7e-14;
4; Mismatches 1;
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Lanthionin Bridged Proteins
                                                                                                                                                      OTHER INFORMATION: Xaa = Hhc: Homohomocysteine
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TITLE OF INVENTION: Lanthionin Bridged Prot
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
                                                                                                                                                                                                                                                 - epsilon-Lysine
OTHER INFORMATION: Synthetic construct
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Query Match
Best Local Similarity
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US-10-131-543-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.9%; Score 148; DB 9; Length 35; Best Local Similarity 85.7%; Pred. No. 7.9e-14; Matches 30; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SNLSTCVLGKLS --- OELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                   LOCATION: 14
OTHER INFORMATION: Xaa - epsilon-Lysine
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 17
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 25, Application US/10131543; Publication No. US20030072709A1; GENERAL INFORMATION:
                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cyr, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: AMIDATION
; LOCATION: 17, 35
US-10-131-543-26
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NAME/KEY: VARIANT
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US-10-131-543-26
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APPLICANT: Pearson, Daniel A.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REFRENCE: 09744-016001
CURRENT APPLICATION NUMBER: US/10/131,543
CURRENT RILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 09/694,992
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WES-10-13-15-643-24

Sequence 24, Application US/10131543

Publication No. US20030072709A1

GENERAL INFORMATION:
APPLICANT: Cyr. John E.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REFERENCE: 09744-01601
CURRENT FILING DATE: 2002-04-92
PRIOR FILING DATE: 2002-04-92
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 24
LENGTH: 35
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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LOCATION: 1, 14
FEATURE:
NAME/KEY: VRIANT
LOCATION: 14
OTHER INFORMATION: beta-Dap: 2,3 diaminopropionic acid residue
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Pred. No. 9e-14;
1; Mismatches 0;
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Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.6%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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85.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 30; Conserva
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; LOCATION: 16, 34
US-10-131-543-25
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Publication No. US20030072709A1

Sequence 12, Application Sequence 12, Application No. US20030072709A1

GENERAL INFORMATION:
APPLICANT: Cyr, John E.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOFTHERS
FILE REPERENCE: 0974-016001
CURRENT APPLICATION NUMBER: US/10/131,543

CURRENT APPLICATION NUMBER: US 09/694,992

PRIOR APPLICATION NUMBER: US 09/694,992

PRIOR APPLICATION NUMBER: PILOF 24

PRIOR APPLICATION NUMBER: PILOF 24

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FRACE FRACE FRACE OF WINDOWS VETSION 4.0

SEQ ID NO 12

LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and second Ser US-09-852-870A-16
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Indels
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                                                                                                                                                                                 Sequence 16, Application US/09852870A
Patent No. US20020165132A1
GENERAL INFORMATION
TITLE OF INFORMATION
FILLE OF INFORMATION
FILLE OF INFORMATION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
                                        3 SNLSTCVLGKLS----QELHKLQTYPRTNTGSGTP 33
                                                            LOCATION: 6
OTHER INFORMATION: Xaa = Hhc: Homohomocysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
30; Conservative
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LOCATION: 13
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Matches
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2: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1981\) DAT:*

3: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1982\) DAT:*

4: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1981\) DAT:*

5: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1981\) DAT:*

6: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1981\) DAT:*

7: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1981\) DAT:*

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11: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1991\) DAT:*

12: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1991\) DAT:*

13: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1991\) DAT:*

14: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1991\) DAT:*

15: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1992\) DAT:*

16: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

17: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

18: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

19: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

20: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

21: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -embl\\ AA1995\) DAT:*

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23: \( SIDS2\) gcgdataJgeneseq\( geneseqp\) -enceeqp\( geneseqp\) -embl\\ AA1995\) DAT:*

23: \( SIDS2\) gcgdataJgeneseq\( geneseqp
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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183
1 mcsnlstcvlgklsgelhklqtyprtntgsgtpg 34
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Fish calcitonin de	Salmon calcitonin Salmon calcitonin-	Sequence of salmon	Partial protein se	Synthetic CT pepti	Salmon calcitonin,	[Met 0] -salmon cal	[Leu 0]-salmon cal	[Met 0, Leu 8]-sal
SUMMARIES	AAP60792	AAP80414 AAP80676	AAP81041	AAB61575		ABG60636	AAR30341	AAR30338	AAR30314
DB	_	ש פ	σ	22	20	23	13	13	13
Length	34	3.4	34	53	33	136	33	33	33
% Query re Match Length DB	100.0	100.0	100.0	100.0	97.3	97.3	96.7	95,1	95,1
Score	183	183	183	183	178	178	177	174	174
Result No.		3 6	4	S	9	7	æ	6	10

[Val 0]-salmon ca Peptide prepd. by Sequence of D-Arg 1,7-di-Sactandio Sequence of N(aLph Sequence of N(aLph Salmon calcitonin Fragment 6 of Sal Salmon calcitonin Calcitonin deriv. Calcitonin deriv. Calcitonin deriv. Calcitonin agonist pe Salmon calcitonin Salmon calcitonin For ole salmon ca [Ser 0]-salmon ca [Na 0]-salmon ca [Leu 0, salmon ca [Leu 0, sel sel sel [Leu 0, leu 8]-sel [Ile 0, Leu 8]-sel	
3 AAR30339 3 AAR30339 AAP20388 AAP40289 AAP71360 AAP71487 AAR36987 AAR36987 AAR59790 5 AAR59790 5 AAR59790 6 AAR86858 6 AAR86858 6 AAR86858 6 AAR86858 6 AAR86432 8 AAR30342 22 AAR30343 22 AAR30343 23 AAR30343 24 AAR30342 23 AAR30343 24 AAR30343 25 AAR30343 26 AAR30343 27 AAR30343 28 AAR30343 28 AAR30343 28 AAR30343 29 AAR303313 20 AAR303313	n; 34 AA. Dualifiers Eptide of claim By be Asn or As Ay be Thr or Va By be Ser or Al 15. 16.
1.55	irst entraderivatifations (1997) Location 2.34 2.34 2.34 2.34 2.34 2.34 2.34 2.34
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This salmon calcitonin protein is produced as a fusion protein. The process can also be used to produce e.g. interferon and proinsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA(ds) encoding salmon calcitonin was synthesised as a single coding strand with a terminal hairpin primer. The complementary strand was synthesised from the primer.

Use of oligonucleotides with a hairpin loop primer avoids the ne for femmically synthesising both strands. Also the filling in stean be performed using labelled nucleotides to give products suitable for use as probes. Mutagenic primers can be used to introduce site specific mutations.

See also AAN81267 and AAN81268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from single strand with terminal hairpin loop by filling in second strand, then opening or removing hair pin
                                                              Length 34;
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                                                                                         Indels
                                                                                                                                                                                                                                                                                                                 3' terminal hairpin loop; double stranded DNA synthesis; salmon calcitonin-Gly 33.\,
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                                                              Query Match 100.0%; Score 183; DB 9; Best Local Similarity 100.0%; Pred. No. 5.4e-17; Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                  1 MCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
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                                                                                                                                                                                                              AAP80676 standard; protein; 34 AA
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                                                                                                                                                                                                                                                                                           Salmon calcitonin-Gly 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1988-339391/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jhlmann E, Hein F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST AG.
                                        34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1988;
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                                                                                                                                                                                                                                                                                                                                                                                    EP292802-A.
                                                                                                                                                                                                                                                                                                                                                            synthetic.
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AAP81041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcitonin; beta-galactosidase; interferon; proinsulin; secretin; inter-leukin-2; hirudin; growth hormone releasing factor.
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                            The sequence encodes a fish calcitonin derivative which may be used for the construction of expression vector pSCT1 capable of transforming an E.coli host for the efficient large scale expression of the product.
                                                                                                                                                                                                Biologically active fish calcitonin contg. extra glycine at C-terminal - convertible to natural form and prepd. using E.coli recombinant transform.
                                                                                                                     Ikushima N;
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                                                                                                                                                                                                                                                                                                                                                                        Length 34;
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                                                                                                                      Saito A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmon calcitonin produced by recombinant methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 MCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
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Matsumoto R, Watanabe K;
                                                                                                                                                                                                                                                 Disclosure; Fig 1; 106pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP80414 standard; protein; 34 AA
                         (SAGA ) SAGAMI CHEM RES CENTRE.
J(ZENG ) CENTRAL GIASS KR.
(HODO ) HODGGAYA CHEMICAL.
(RIPE) NIPPON SODA KR.
(NISC ) NISSAN CHEMICAL INDS LTD.
(TOYJ ) TOYO SODA MFG KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88EP-0105438;
 85JP-0113254.
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88DE-3712361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wetekam W, Jansen HW,
                                                                                                                                                          WPI; 1986-068975/10.
N-PSDB; AAN60710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-294356/42.
N-PSDB; AAN80970.
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                                                                                                                                                                                                                                                                                                                                               34 AA;
 28-MAY-1985;
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19-FEB-1988;
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                                                                                                                                                                                                                                                                                                                                               Sequence
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Pri "Madard; protein; 34 AA.

Sequence of salmon calcitonin I having an additional C-terminal glycine. Hypocalcaemic; hypophosphateamia peptide hormone; pancreatitis therapy.

Uhlmann E; Muller H,

Salmon calcitonin I derivs. prepn. . by inserting new plasmid encoding for the deriv. into e.g. Bscherichia coll gene

Calcitonin is a hypocalcaemic and hypophosphataemia peptide hormone which regulates serum levels of Ca. It is useful for treating Ca metabolic disorders, as an analgesic and for treating acute pancreatitis inhibiting enzyme secretion.

Gaps ·; Length 34; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 34; Conservative 0; Mismatches 0;

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AAB61575 standard; Protein; 53 AA AAB61575;

(first entry) 03-APR-2001 Partial protein sequence of pCLYSM.

Transgenic; milk; lysozyme; pCLYSM; salmon; calcitonin.

Unidentified.

WO200100855-A1.

04-JAN-2001

23-JUN-2000; 2000WO-GB02459.

99GB-0014733. 23-JUN-1999; 10-AUG-1999;

(PPLT-) PPL THERAPEUTICS SCOTLAND LTD.

McCreath GE;

WPI; 2001-137958/14. N-PSDB; AAF28653.

Producing peptides for use as medicaments, nutritional additives or research tools, comprises expressing a fusion protein, which contains the peptide linked to a lysozyme fusion partner protein, in the milk of a transgenic mammal

Example 1; Fig 1; 57pp; English.

The present invention relates to a method for producing a peptide. The method comprises expressing in the milk of a transgenic non-human placental mammal a fusion protein, comprising the peptide to be expressed linked to lysozyme (a fusion partner protein). The method is useful for producing proteins or peptides that are useful as medicaments, untritional additives or research tools. The present sequence is a nutritional additives or research tools. The present sequence is a nutritional additives or research tools. The present sequence is a nutritional additives or research tools. The present sequence is a nutritional additives or tesaerch tools. The present sequence is a nutritional additives or tesaerch tools. The present sequence is a numble. The fusion protein in the milk of transgenic animals. The fusion protein in the milk of transgenic canning the fusion protein in the milk of transgenic canning the order products of a linker arm fused to the lysozyme cterninal by cyanogen bromide chemical cleavage pitch of the lysozyme gene, peptide linker (see AABE1572). CNBr cleavage site and salmon calcitonin coding sequence, ovine BLG 3' over the protein and the putla Buttal Bussind vector. The present sequence is a partial protein sequence of pCLXSM comprising the peptide linker, the CNBr cleavage site and the calcitonin peptide sequence.

Sequence

Gaps ó: Length 53; Indels Query Match 100.0%; Score 183; DB 22; Best Local Similarity 100.0%; Pred. No. 8.7e-17; Matches 34; Conservative 0; Mismatches 0;

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ŏ g RESULT 6 ABB08914

; 0

ABB08914 standard; peptide; 33 AA

16-JUL-2002 (first entry)

Synthetic CT peptide sCT(Gly).

TNF; tumour necrosis factor; beta-sheet; fusion protein; recombinant production; Escherichia coli; TNF fusion vector; pT7-T150; pT7-T57; CT; sCT; pT150-sCT(Gly).

Synthetic.

KR133475-B1.

94KR-0007018. 04-APR-1994; 21-APR-1998

94KR-0007018. 04-APR-1994; (HANI-) HANIL SYNTHETIC FIBER CO LTD.

Kang S; Shin H, Jang S, Kim D,

WPI; 1999-617508/53.

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Gaps

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Indels

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Query Match Best Local S: Matches 33, Sequence

RESULT 7

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ligand that confers transcellular, transcytotic or paracellular transporting properties to an agent specifically bound to the ligand, where (II) is not an antibody. Alternatively, (I) comprises two or more (II) directed to one or more ligands. (I) is useful for delivering a biologically active agent to an animal, for transporting an active agent thereof or mucosal barrier, and for treating or active agent through an epithelial or mucosal barrier, and for treating or active agent dentifying disease in an animal e.g. diseases of the respiratory system including lung cancer and tumours, asthma, pathogenic infections, allergy-related disorders, gastrointestinal tract disorders, disorders and any disease or disorder involving polyimmunosquolulin receptor (pigR) displaying cells. This is the amino acid sequence of a protein associated with the transport of biologically active agents across cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sCT; calcium regulation; thyroid gland; hormone; bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New synthetic calcitonin peptide(as) are hypocalcaemic agents -
for treating Paget's disease, osteoporosis, bone fracture, etc.
with lower immunogenicity than natural calcitonin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This hypocalcaemic peptide is an example of novel calcitonin analogues which have amino acid additions at the N-terminal which, alone or with other substitutions, and with deletions at other residues, act to improve potency, prolong duration of the hormonal effect and increase oral or nasal
                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 23; Length 136;
Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "designated position 0, N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                      97.3%; Scole ...
100.0%; Pred. No. 1.1.
*'''A 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100. 33; Conservative
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                                                                                                                                                                                                                                                                                                                                       136 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1991;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complex useful for transporting active agent through epithelial barrier, has biologically active portion and target element directed bligand that confers e.g. transcytchic properties to agent specific to Agand
                                                                                                                                   The invention relates to a method for the recombinant production of protetars, involving the fusion of a leader sequence capable of forming a beta-sheet to a desired protein. In particular, a protein of interest is expressed in Escherichia coli as a fusion with a beta-sheet forming portion of human tumour necrosis factor (TNF; see ABB08912), and the TNF fusion vectors pT7-T150 and pT7-T57 are used to accomplish this. The present sequence represents a synthetic CT (not defined) peptide designated sCT(Gly), which is a component of the TNF-SCT(Gly) fusion protein encoded by the TNF fusion vector pT150-SCT(Gly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yon described a complex or compound (I) comprising a ractive portion and a target element (II) directed to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                         Use of beta-sheet forming amino acid leader sequence for the production of proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%; Score 178; DB 20;
100.0%; Pred. No. 2.4e-16;
tive 0; Mismatches 0;
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                                                                                            Example 3-A; Page 7; 14pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG60636 standard; Protein; 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000; 2000US-237929P.
13-NOV-2000; 2000US-248478P.
14-NOV-2000; 2000US-248819P.
09-FEB-2001; 2001US-267601P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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N-PSDB; ABK81195.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                33 AA;
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Sequence 33 AA;

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ö 0; Gaps Length 33; 0; Indels Match 96.7%; Score 177; DB 13; Local Similarity 100.0%; Pred. No. 3.2e-16; les 33; Conservative 0; Mismatches 0; Query Match Best Loc Matches δ

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RESULT 9

Ä AAR30338 standard; peptide; 33 AAR30338; [Leu 0]-salmon calcitonin.

30-APR-1993 (first entry)

sCT; calcium regulation; thyroid gland; hormone; bone resorption.

Salmon.

_note= "designated position 0, i.e. additional N-terminal amino acid " $% \left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right) =\frac{1}$ Location/Qualifiers Key Misc-difference

2..8 Disulfide-bond Modified-site

/note= "amidated"

10-DEC-1992.

92WO-US04854. 03-JUN-1992; 910S-0711180. 05-JUN-1991;

(VICA-) VICAL INC.

Basava C, Hostetler KY;

WPI; 1992-433374/52.

New synthetic calcitonin peptide(as) are hypocalcaemic agents -for treating Paget's disease, osteoporosis, bone fracture, etc. with lower immunogenicity than natural calcitonin(s) Claim 3; Page 28; 42pp; English.

This hypocalcaemic peptide is a specifically claimed example of Cacittonin analogues which have amino acid additions at the N-terminal which, alone or with other substitutions, and with deletions at other residues, act to improve potency, prolong duration of the hormonal effect and increase oral or masal bioavallability, c.f. native CTs. The analogues can be used to reduce or normalise serum calcium levels or to influence bone metabolism. They are thus useful for treating e.g. Vitamin D intoxication, hyperparathyroidism, idiopathic hypercalcaemia of infancy, bone fracture, rickets, osteoporosis and bone pain.

Gaps This hypocalcaemic peptide is an example of novel calcitonin and analogues which have amino acid additions at the calcitonin analogues which have amino acid additions at the deletions at other residues, act to improve potency, prolong duration of the hormonal effect and increase oral or masal bioavailability, c.f. native CTs. The analogues can be used to reduce or normalise serum calcium levels or to influence bone metabolism. They are thus useful for treating e.g. vitamin D intoxication, hyperparathyroidism, idiopathic hypercalcaemia of infancy, bone fracture. rickets, osteoporosis and bone pain associated with these diseases or with articular rheumatism. The peptides also inhibit gastrin secretion making them useful to sCT; calcium regulation; thyroid gland; hormone; bone resorption. New synthetic calcitonin peptide(as) are hypocalcaemic agents - for treating paget's disease, osteoporosis, bone fracture, etc. with lower immunogenicity than natural calcitonin(s) 0; /note= "designated position 0, i.e. additional N-terminal amino acid " associated with these diseases or with articular rheumatism. T peptides also inhibit gastrin secretion making them useful to treat acute pancreatitis and gastrointestinal disorders, esp. gastric ulcers. 95.1%; Score 174; DB 13; Length 33; 97.0%; Pred. No. 8e-16; Live 1; Mismatches 0; Indels /note= "designated position 8 in sCT, Leu replaces Val" 1 MCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33 1 LCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33 Location/Qualifiers 1 Example 16c; Page 28; 42pp; English. AA. 33 /note= "amidated" [Met 0, Leu 8]-salmon calcitonin. AAR30314 standard; peptide; 33 92WO-US04854. 91US-0711180. 30-APR-1993 (first entry) Best Local Similarity 97.03 Matches 32; Conservative Basava C, Hostetler KY; Misc-difference 9 WPI; 1992-433374/52. (VICA-) VICAL INC. 33 AA; Misc-difference Modified-site 03-JUN-1992; 05-JUN-1991; W09221369-A. Sequence AAR30314; Query Match Salmon. RESULT 10 AMANAGONAL
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Length 33; Indels

Score 173; DB 13; Pred. No. 1.1e-15; 1; Mismatches 0;

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94.5%;
97.0%;
      Query Match
Best Local Similarity 97.0
Matches 32; Conservative
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Modified-site
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AAR30340
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for treating Paget's disease, osteoporosis, bone fracture, etc.
with lower immunogenicity than natural calcitonin(s)
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treat acute pancreatitis and gastrointestinal disorders, esp. gastric ulcers.
                                                                                    Length 33;
                                                                                                                        Indels
                                                                                Ouery Match 95.1%; Score 174; DB 13; Best Local Similarity 97.0%; Pred. No. 8e-16; Matches 32; Conservative 1; Mismatches 0;
                                                                                                                                                                       1 MCSNLSTCLLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                    1 MCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                     AAR30339 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "amidated"
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                                                                                                                                                                                                                                                                                                                                                                      [Val 0]-salmon calcitonin.
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                                                  33 AA;
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Modified-site
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AAR30339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sCT; calcium regulation; thyroid gland; hormone; bone resorption.
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for treating Paget's disease, osteoporosis, bone fracture, etc.
with lower immunogenicity than natural calcitonin(s)
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94.5%: Score 173; DB 13; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.1e-15;
Matches 32; Conservative 1; Mismatches 0; Indels
1 MCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                       1 VCSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                 AAR30340 standard; peptide; 33 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               [Ile 0]-salmon calcitonin.
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Sequence of D-Arg (24) salmon calcitonin deriv.
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        NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 Membered polypeptide chain - obtd. by reacting 24 and 4 membered peptide(s) in the presence of trypsin
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94.0%; Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= protected /note= "with H or thiol protecting gp." Disulphide_bond 1..7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= protected /note= "with H or thiol protecting gp."
                                                                                                                                                                                                                                                                              Peptide prepd. by reaction in the presence of trypsin.
        Trypsin; thiol; trypsin-like proteinase.
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                                                                                                                                            peptide; 32 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SAGA ) SAGAMI CHEM RES CENTRE. (TEIK ) TEIKOKU HORMONE MFG LID.
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86ES-0556432.
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Modified-site
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23-JUN-1986;
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                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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AAP40289 standard; protein; 32 AA.

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14-JAN-1992 (first entry)

AAP40289; RESULT 14
AAP40289
ID AAP40:
XX
AC AAP40:
XX
DT 14-JAI

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Orlowski RC, Seyler JK, Colescott RL, Stahl GL, Enkoji T, Geever JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cyclic disulphide peptides of the invention have calcitonin activity. They are prepd. by standard solid phase peptide synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,7-di-S-acetamidomethyl [1,7-di-Cys(Acm)] salmon calcitonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-arginine (24) salmon and eel calcitonins and intermediates have calcitonin hormone activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
94.0%; Score 172; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels
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AAP71360
ID AAP71360 standard; peptide; 32 AA.
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; column 18; 4pp; English.
                                                                                                                                                                                              /label= Pro-NH2
                                                                                                     Tabel= H-Cys
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                                                                                                                                                          label- D-Arg
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Hormone; calcitonin analogue.
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                                                                                                                     Disulfide-bond
Modified-site
                                                                    Key
Modified-site
                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                      24-SEP-1982;
                                                                                                                                                                                                                                                                                                                                        24-SEP-1982;
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                                                                                                                                                                                                                                                                   04-SEP-1984.
                                  Salmo salar.
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WPI; 1987-129186/18.

New salmon and eel calcitonin analogues \cdot do not have disulphide bond connecting cysteine residues.

Claim 1; page 9-10; 10pp; English.

The salmon calcitonin analogue has the biological activity of the same type of calcitonin and comparable potency to known calcitonins. It differs in not having a disulphide bond connecting the cysteines at positions 1 and 7. In a test, 3 and 9 MU/100 g body weight of the standard salmon calcitonin and 0.2 ml/100 g body weight of the standard salmon calcitonin and 0.2 ml/100 g body weight of the analogue were given to different rates. Serum calcitum was determined after 1 hr. The standard salmon calcitonin was found to contain 4000 IU/mg, whereas the analogue assayed at 4250 IU/mg.

Sequence 32 AA;

;0 Ouery Match 94.0%; Score 172; DB 8; Length 32; Best Local Similarity 100.0%; Pred. No. 1.4e-15; Matches 32; Conservative 0; Mismatches 0; Indels

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Search completed: May 30, 2003, 09:50:26 Job time: 37 secs

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May 30, 2003, 09:49:44; Search time 15 Seconds Run on:

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SEQ1 183 1 mcsnlstcvlgklsqelhklqtyprtntgsgtpg 34

score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

1: pirl: * 2: pirl: * 3: pir2: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	,		•				•	0.					10	7	***			O.	10				10	8	m	-	3	.0	0	3
SUN	QI	151029	151260	TCON	TCEE	TCONZ	TCONSC	TCONZE	TCCH	TCONS	TCRT	TCHU	A41716	JC4977	A35934	A60063	TCSH	80208	T12436	TCBO	TCPG	S16583	S16583	S1574	862453	AD2321	T06463	AG1026	B25750	A6971
	DB	~	~	-	Н	1	н	~		1	~	7	~	7	~	N	-1	7	N	7	Н	7	~	~	7	7	7	7	~	7
	Query Match Length	26	59	136	32	32	32	32	138	32	136	141	141	136	137	67	143	402	397	32	32	395	404	404	438	334	352	664	213	401
œ	Query	97	97.3	97.3	86.9	85.8	85.8	85.8	85.8	84.2	59.0	55.2	55.2	54.6	52.5	49.2	39.3	37.2	36.6	33.9	33.3	33.3	33.3	33.3	31.7	31.1	31.1	0	29.8	on .
	Score	178	178	178	159	157	157	157	157	154	108	101	101	100	96	90	72	68	29	62	61	61	61	61	28	57	57		54.5	4
	Result No.	-	7	ю	4	J.	9	7	œ	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	53

type II site-speci	DNA topoisomerase	phosphoribulokinas	alpha-2-antiplasmi	conjugal transfer	hypothetical prote	hypothetical prote	DNA topoisomerase	eae protein (enter	transposase - Kleb	hypothetical prote	hypothetical prote	rec15 protein - fi	NADH2 dehydrogenas	B. subtilis transc	cysteine synthase/
A81166	H69724	T08167	847217	B82606	T27904	T46443	A82638	141197	538653	H71836	G70841	S70725	A84948	AD1130	G82247
7	~	~	7	~	~	7	7	7	ď	7	7	~	~	7	7
489	727	375	491	685	431	435	619	686	952	352	159	180	224	309	355
ഗ	8.7	28.4	27.9	27.9	27.6	27.6	26.8	26.8	26.8	26.5	26.3	26.2	26.2	26.2	26.3
29.	ď	• •													
54 29.		52		51	50,5	50.5	49	49	49	48.5	48	48	48	48	48

ALIGNMENTS

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calcitonin 1 - pink salmon (fragment)
calcitonin 1 - pink salmon (fragment)
calcitonin 1 - pink salmon (fragment)
c)species; oncorphynchus gorbuscha (pink salmon)
c)spate: 13-5ep-1996 #sequence_revision 13-5ep-1996 #text_change 16-Jul-1999
C)Accession: 151029; $42985
FNATTial, K.; Muubras, L.; Taboulet, J.; Jullienne, A.; Berry, M.; Milhaud, G.; Bens Proc. Natl. Acad. Sci. U.S.A. 91, 4912-4914, 1994
A)Title: The calcitonin gene is expressed in salmon gills.
A)Reference number: 151029; MUID:94255438; PMID:8197156
A)Recession: 151029
A)Rolecule Type: mRNA
A)Recidues: 1-56 <MRN>
A)Recidues: 1-56 <MRN>
A)Cross references: EMBL:X78080; NID:9459540; PIDN:CAA554988.1; PID:9459541
C)Genetics:
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C; Superfamily; calcitonin
F:1-56/Product: procalcitonin 1 (fragment) #status predicted <MAT1>
F:3-34/Product: calcitonin 1 #status predicted <MAT2>
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Best Local S.
Matches 33,
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2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34 qq δy

RESULT 2
151260
calcitonin I - pink salmon (fragment)
cispecies: Oncorhynchus gorbuscha (pink salmon)
C;species: Oncorhynchus gorbuscha (pink salmon)
C;species: Oncorhynchus gorbuscha (pink salmon)
C;species: 151260; Beguence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151260; Island
C;Accession: 151260; Mulpi 9504
A;Ittle: Production of salmon calcitonin I in Oncorhynchus gorbuscha by alternative p
A;Accession: 151260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 151261
A;Residues: 1-59 4MAR>
A;Cross references: GB:S74352; NID:g786497; PIDN:AAD14151.1; PID:g4261851
A;Accession: 151261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 151261
A;Accession: 151261
A;Accession: 151262
A;Genesics: 1-59 4MAR>
A;Cross references: GB:S74353; NID:g786498
A;Cross references: GB:S74353; NID:g786498
A;Cross references: GB:S74353; NID:g786498

δ qa

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calcitonin 2 - chum salmon
Cispecias: Oncorbypthus keta (chum salmon)
Cispecias: Ja-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Aug-1996
CiAccession: CO1531, Ad1531
R.Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr., In Endocrinology 1971: Proceedings of the calcitonins: some recent advances.
A.Ritle: Chemistry and physiology of the calcitonins: some recent advances.
A.Rocession: CO1531
A.Rocession
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Byless, J. 32 (KED)
Ryless, J. Bauer, W. Bossert, H.; Zehnder, K.; Guttmann, S.
Wature New Biol. 240, 62-83, 1972
Anotecule type: protein type to the same as the natural ones on the scene number: A93406; MUID: 73047885; PMID:4508400
Anotecule synthetic primones were the same as the natural ones on the natural to the synthetic primones were the same as the natural ones on the control to the synthetic primones were the same as the natural ones on the control to the synthetic primones were the same as the natural ones on the control to the synthetic primones were the same as the natural ones on the control to the synthetic primones were the same as the natural ones on the control to the synthetic primones and the synthetic carboxyl end; hormone
Fill/Niulfide bonds: #status experimental
Fill/Millified site: amidated carboxyl end (Pro) #status experimental
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C;Keywords: amidated carboxyl end; hormone
C;Keywords: amidated carboxyl end; hormone
F;1-7/Disulfiled bonds: #status experimental
F;32/Modified site: amidated carboxyl end (Pro) #status experimental
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                                                 Length 32;
                                     Query Match

Query Match

86.9%; Score 159; DB 1; Length 32

Best Local Similarity 90.6%; Pred. No. 2.2e-15; Indels Matches 29; Conservative 2; Manaches 1; Indels
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Pred. No. 4.1e-15;
3; Mismatches 1; Indels
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es 28; Conserv
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Best Local Si
Matches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGON Calcitonin | precursor - salmon |
C:Sepectes: Onocrhynchus Sp. (salmon) |
C:Sepectes: D. (salmon) |
C:Sepectes:
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A. Realduss: 1.32 < NODD
C. Superfamily: calcitonin
C. Keywords: amidated carboxyl end
F.1.7/Disulfide bonds: #status experimental
F.32/Modified site: amidated carboxyl end (Pro) #status experimental
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                                                                                                         Length 59;
                                                                                                                                                                                                      Indels
                                                                                                   Query Match 97.3%; Score 178; DB 2; Best Local Similarity 100.0%; Pred. No. 8.8e-18; Marches 33; Conservative 0; Mismatches
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C, Superfamily: calcitonin
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Wichtelms: Amountains amino-terminal procalcitonin cleavage peptide (N-procT); carboxyl-termina C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Sate: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 18-Jun-1999
C; Accession: A94259; A98853; A91238; I55221; I52379; A01525
R; Jacobs, J.W.; Goodman, R.H.; Chin, W.W.; Dee, P.C.; Habener, J.F.; Bell, N.H.; Pott Science 213, 457-459, 1981
A; Reference number: A94259; MUID:81225842; PMID:6264603
A; Reference number: A94259; MUID:81225842; PMID:6264603
A; Molecule type: mRNA
A; Residues: 1-136 < JAC>
                                                                                                                                          A;Cross-references: GB:M27563; NID:9211373; PIDN:AAA48648.1; PID:9211374 C;Comment: The calcitonin gene codes for two mRNA species by tissue-specific alternat ripheral nervous system codes for calcitonin gene-related peptide. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation; synthesis A; Note: the synthetic hormones were the same as the natural ones on the basis of phys an calcitonins 1 or 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rikeutmann, H.T.; Lequih, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr., in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S., A;Title: Chemistry and physiology of the calcitonins: some recent advances. A;Reference number: A04616
A;Accession: B01531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                              A; Introns: 29/2; 73/2
C; Superfamily: calcitonin
C; Superfamily: calcitonin
C; Superfamily: calcitonin
F; 82-113/Product: calcitonin #status experimental <MAT>
F; 82-88/Disulfide bonds: #status experimental
F; 813/Modified site: amidated carboxyl end (Pro) (amide in mature form from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcitonin 3 - coho salmon
C.Species: Oncorhynchus Kisutch (coho salmon)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 08-Dec-1995
C;Accession: B01531; A01531
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C.Keywords: amidated carboxyl end
C:Keywords: amidated carboxyl end
F:1-7/Disulfide bonds: *status experimental
F:32/Modified site: amidated carboxyl end (Pro) *status experimental
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Pred. No. 1.1e-14;
4; Mismatches 1; Indels
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A;Residues: 1-32 <KEU>
Fyless, J.; Bauer, Bossert, H.; Zehnder, K.; Guttmann,
Nature New Biol. 240, 62-63, 1972
A;Title: Synthesis of two natural salmon calcitonins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62-63, 1972
two natural salmon calcitonins
13406; MUID:73047885; PMID:4508400
   A; Reference number: I50182; MUID:85102042; PMID:3838160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 157; DB 1;
Pred. No. 1.7e-14;
4; Mismatches 1;
                                                            A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 71-117 <LA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.8%;
84.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.8
Best Local Similarity 84.8
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                       Gispecies: Oncorthynchus gorbuscha (pink salmon)
Cispecies: Oncorthynchus gorbuscha (pink sequence_revision 31-Dec-1990 #text_change 23-Aug-1996
Cispecies: Dolfs1: And Olfs1: A.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr., J.T.
In Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S., ed. A; Reference number: A04616
A; Reference number: A04616
A; Reference number: A04016
A; Reference number: A04006
A; Reference number: A93406; MUID: 73047885; PMID: 4508400
A; Reference number: A93406; MUID: 73047885; PMID: 4508400
A; Nontents: annotation; synthesis
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A; Residues: 1-32 < HGW>
R; Lassmoles, F.; Jullienne, A.; Desplan, C.; Milhaud, G.; Moukhtar, M.S.
FEBS Lett. 180, 113-116, 1985
A; Title: Structure of chicken calcitonin predicted by partial nucleotide sequence of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: DNA
A; Residues: 1.138 c4M19
A; Residues: 1.138 c4M19
A; Cross-references: EMBL:X06311
A; Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the A; Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the A; Note: the authors translated the codon GAC for residue 56 as Glu; the codon GAC was cc EMBO J. 4, 2603-2607, 1985
A; Miller: Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evide A; Accession: A25725; MUID:86030240; PMID:4054101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcitonin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C;Accession: S00153; A25725; A24415; IS0182; A22467
R;Minvielle, S; Cressent, M.; Delehaye, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.;
FEBS Lett. 223, 63-68, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of chicken calcitonin
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A; Residues: 12-55, E',57-138 <LAS>
A; Cross-references: EMBL: X03012; NID: 963157; PIDN: CAA26796.1; PID: 963158
A; Diochem. 100, 459-467, 1986
A; Title: Isolation and determination of the amino acid sequence of chicker
A; Reference number: A24415; MUID: 87057104; PMID: 3782060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;32/Modified site: amidated carboxyl end (Pro) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
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Pred. No. 4.1e-15;
3; Mismatches 1;
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2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an calcitonins 1 or 2
C. Superfamily: calcitonin
C. Keywords. a midated carboxyl end; hormone
F:1-7/Disulfide bonds: #status experimental
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ilarity 87.5%;
Conservative
                                                                                                                                                                                                                        calcitonin 2 - pink salmon
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es 28; Conserv
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Matches
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δ
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A; Molecule type: mRNA
A; Molecule the authors translated the codon CAG for residue 19 as Glu
R; Edbrooke, M.R.; Parker, D.; McVey, J.H.; Riley, J.H.; Sorenson, G.D.; Pettengill, O
EMBO J. 4, 715-724, 1985
A; Fitle: Expression of the human calcitonin/CGRP gene in lung and thyroid carcinoma,
A; Reference number: A91034; MUID:85230541; PMID:2408883
                                                             Asymptics receipt and methylation of the human calcitonin/alpha-CGRP gene.

A;Title: Structure and methylation of the human calcitonin/alpha-CGRP gene.

A;Reference number: S07643; MUD:89386053; PMID:2571128

A;Recession: S07643; MUD:89386053; PMID:2571128

A;Recession: S07643; MUD:89386053; PMID:2571128

A;Robecule type: DNA

A;Recession: L41 < ARR

A;Reference: EMBL:X15943

A;Robecule type: DNA

A;Reference: EMBL:X15943

A;Reference: EMBL:X15943

A;Reference: EMBL:X15943

A;Reference: CR: Kawashima: E: Semon, D:; Swanson, L.W.; Mermod, J.J.; Evans, Proc. Natl. Alternative RNA processing events in human calcitonin/calcitonin gene-relate

A;Reference number: A94030; MUID:85166259; PMID:3872459
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A; Residues: 121-141 <CON>
R;Craig, R.K.; Riley, J.H.; Edbrooke, M.R.; Broad, P.M.; Foord, S.M.; Al-Kazwini, S.J
Blochem. Soc. Symp. 52, 91-105, 1986
A; Title: Expression and function of the human calcitonin/alpha-CGRP gene in health an
A; Reference number: 139387; MUID:87213363; PMID:3034287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-91, "1', 93-141 <JON>
A; Residues: 1-91, "1', 93-141 <JON>
A; Cross-references: 191, "1', 92-141 <JON>
A; Cross-references: 191, "1', 93-141 <JON>
A; Note: the authors translated the codon AGC for residue 76 as Arg
R; le Moullec, J.M.; Jullienne, A.; Chenais, J.; Lasmoles, F.; Guliana, J.M.; Milhaud, FBBS Lett. 167, 93-97, 1984
A; Title: The complete sequence of human preprocalcitonin.
A; Reference number: S07238; MUID: 84132556; PMID: 6546550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Moseduce type: mRNA
A; Mesdiduce; 1-141 - AMOUD
A; Cross references: EMBL: X00356; NID: 929605; PIDN: CAA25103.1; PID: 929606
B; Rilley, J. H.; Edbrooke, M.R.; Craig, R.K.
R; Rilley, J. H.; Edbrooke, M.R.; Craig, R.K.
A; Rilley, L. 198, TJ-79, 1986
A; Title: Ectopic synthesis of high Mr calcitonin by the BEN lung carcinoma cell line
A; Reference number: S07242; MUID: 86164952; PMID: 3485540
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A; Meaidues: YV; 50.141 (EDB>
A; Meaidues: YV; 50.141 (EDB>
A; Cross-references: GB:X02330; NID:g29607; PIDN:CAA26189.1; PID:g29608
A; Cross-references: GB:X02330; NID:g29607; PIDN:CAA26189.1; PID:g29608
A; Bracq, S.; Machairas, M.; Clement, B.; Pidoux, E.; Andreoletti, M.; Moukhte; FBBS Lett. 331, 15-18, 1993
A; Title: calcitonin gene expression in normal human liver.
A; Reference number: S36900; MuID:94009627; PMID:8405394
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 17-91, 1, 93-141 (ERA>
A; Molecule type: mRNA
A; Residues: 21, 1900-1905, 1968
A; Title: Monschliches calcitonin. III. Struktur von calcitonin M und D.
A; Reference number: A91629; MUID:72162720; PMID:5760861
A; Molecule type: protein
A; Residues: 85-116 (NE)
A;
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A;Residues: 1-141 <RES>
A;Cross-references: GB:M26095; NID:g177965; PIDN:AAA35501.1; PID:g177966
                                    6999-7011, 1989
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A.Cross-references: GB.M31027: GB.J00707: GB.J00708; GB.J00709; GB.M00002: NID:9343161:
R.Marlan Characterization of Tar. Califolds A.G., Nos. B.A.; Evans. R.M.
A.TILLE Characterization of Tar. Califolds and the Characterization of Tar. A.TILLE: Procalifolds and the Characterization of Tar. A.TILLE: Procalifolds and the Characterization of Norgental and the Characterization of Tar. A. Tar. Califolds and the Characterization of Norgental and A.M. Medical Characterization of Norgental A.M. Medical Ch
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C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 11-Aug-1995 #text_change 08-Dec-2000
C;Accession: S07643; C22949; S07238; S07242; A91034; S36900; A91629; A60784; I39387; I65
R;Broad, P.M.; Symes, A.J.; Thakker, R.V.; Craig, R.K.
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Pred. No. 1.2e-07;
7; Mismatches 8;
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ilarity 54.5%;
Conservative
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Best Local Similarity
Matches 18; Conserv
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29607; PIDN:CAA26189.1; PID:929608 B.; Pidoux, E.; Andreoletti, M.; Moukhtar, M.S.;

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C;Accession: A60063
R;Mol, J.A.; Kwant, M.M.; Arnold, I.C.J.; Hazewinkel, H.A.W.
Regul, Peptr. 35, 189-195, 1991
A;Title: Elucidation of the sequence of canine (pro)-calcitonin. A molecular biologic A;Reference number: A60063; MUID:92100867; PMID:1758974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcitonin and katacalcin peptides
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A; Rosidues: 1.67 (WOLD-
A) Cross-references: GB: X56994
C; Superfamily: calcitonin
C; Keywords: amidated carboxyl end; hormone; thyroid gland
E; 22-53, Product: calcitonin #status predicted <MAT>
F; 53/Modified site: amidated carboxyl end (Pro) (amide in mature form from following
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 20-Jun-2000
C; Accession: JC4977.
B; Rehli, M.; Luger, K.; Beier, W.; Falk, W.
Biochem. Biophys. Res. Commun. 226, 420-425, 1996
A; Title: Molecular cloning and expression of mouse procalcitonin.
A; Reference number: JC4977; MUID:96400274; PMID:8806650
A; Accession: JC4977
A; Molecule type: MRA
A; Residues: 1-136 < REB
A; Residues: 1-136 < REB
A; Cross-references: EMBL:X97991; NID:91644303; PIDN:CAA66630.1; PID:91644304
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Cispecies: Oryclolagus cuniculus (domestic rabbit)
Cispecies: Oryclolagus cuniculus (Gracesion: A55934
Cispecies: Oryclolagus cuniculus (Gracesion: A): Segond, N.; Milhaud, G.; Lasmol Biochem: Biochem: Biochem: Diophys: Res. Commun: 171, 1111-1114, 1990
A):Title: Predicted structure of rabbit N-terminal, calcitonin and katacalcin A):Reference number: A35934; MUID:91024969; PMID:1699521
A):Accession: A35934
A):Molecula type: MRNA
A):MOLecula type
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C;Species: Canis lupus familiaris (dog)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.5e-06;
7; Mismatches 9;
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51.5%; Pred. No. 5.6e-06;
tive 6; Mismatches 10;
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51.5%; Pred. No. 1.9e-05;
Live 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |||||||||| :||:|| || || || || || || 85 CGNLSTCMLGTYTQDLNKFHTFPQTSIGVEAPG 117
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51.5%;
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Best Local Similarity 51.59
Matches 17; Conservative
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les 17; Conservative
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C; Superfamily: calcitonin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Modecule type: mRNA
A; Residues: 1-141 <MIN>
A; Residues: 1-141 <MIN>
A; Cross-references: GB: M64486; NID: 9179819; PIDN: AAA58403.1; PID: 9179820
A; Experimental source: meduliary thyroid carcinoma
A; Note: production of calcitonin carboxyl-terminal peptide II was demonstrated in medull C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
R;Nelkin, B.D.; Rosenfeld, K.I.; de Bustros, A.; Leong, S.S.; Roos, B.A.; Baylin, S.B. Biochem. Biophys. Res. Commun. 123, 648-655, 1984
A;Title: Structure and expression of a gene encoding human calcitonin and calcitonin gen A; Reference number: 152204; WUID:85022523; PMID:6148938
A;Accession: 165199
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F.85-116/Product: calcitonin #status experimental <CTN>
F:121-141/Product: calcitonin carboxyl-terminal peptide II #status experimental <CCII>
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A; Residues: 48-83 <RE2>
A; Cross-references: GB: K03513; NID: 9181173; PIDN: AAA52124.1; PID: 9553244
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Pred. No. 1.2e-06;
6; Mismatches 10;
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Pred. No. 1.2e-06;
6; Mismatches 10
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A;Cross-references: GDB:120571; OMIM:114130
A;Map position: 11p15.2-11p15.1
C;Superfamily: calcitonin
                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 51.5%; Pre
Matches 17; Conservative 6;
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51.5%;
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ò QQ Search completed: May 30, 2003, 09:51:17 Job time : 16 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 30, 2003, 09:49:44; Search time 79 Seconds (without alignments) 88.679 Million cell updates/sec Run on:

Perfect score: Title:

183 1 mcsnlstcvlgklsgelhklqtyprtntgsgtpg 34 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

SPTREMBL_21:* Database

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_bacteriap:* sp_organelle:* sp_phage:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* sp_plant:*
sp_rodent:*
sp_virus:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

SUMMARIES

ID Description	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	091970 091970 oncorhynchu	092163	089984	Q8QG82 Oncorhynchu						Q8QFT8 Q8qft8 fuqu rubrip			Q9W6Z3 qallus qall		
% Query Match Length DB	56 13	59 13	62 13	32 13	32 13	32 13	32 13	32 13	32 13	32 13	136 13	32 13	62 13	65 13	50 13	740
% Query Match I	97.3	97.3	97.3	94.0	94.0	94.0	94.0	94.0	94.0	92.3	7.06	86.9	86.3	85.8	85.2	נוא
Score	178	178	178	172	172	172	172	172	. 172	169	166	159	158	157	156	113
Result No.	! ! ! !	2	6)~	S	9	7	80	6	10	11	12	13	14	15	אר

Q13935 homo sapien	O88610 mus musculu	Q9myv2 canis famil			P93681 pisum sativ	Q9atc3 vaucheria 1	Q9rhf5 salmonella	Q9xaz6 neisseria m	Q9k091 neisseria m	Q9bgwl macaca fasc	Q8q805 human immun	Q9cnf6 pasteurella	Q9d9d4 mus musculu	P96583 bacillus su	Q98871 brachydanio	O35255 mus musculu	Q99190 mus musculu	Q96ev5 homo sapien	Q9pbt0 xylella fas	Q8rnq8 legionella	Q8szz7 drosophila	Q9v358 drosophila	Q9nif9 metacnephia	Q9nta2 homo sapien	Q23526 caenorhabdi	Q937b7 pseudomonas	Q8rsh4 uncultured	Q8s8p8 arabidopsis
013935	. 088610	Q9MYV2	095033				Q9RHF5	Q9XAZ6	5 Q9K091	Q9BGW1			Q9D9D4	5 P96583	3 098871	035255	067660	Q96EV5		Q8RNQ8	Q8SZZ7	Ø9V358	Q9NIF9	Q9NTA2	023526	Q937B7	Q8RSH4	088888
93 4	48 11	130 6	7	~	Н	405 10	664 16	473 2	489 16	103 6	233 15	Н	310 11	727 16	321 13	462 11	462 11	164 4	685 16	1066 2	1332 5	1472 5	152 5	435 4	439 5	687 2	687 2	83 1(
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17	18	19	20	21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
                                                                                                                                                         Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8017;
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                                                                                                                                                                                                                                              | SEQUENCE FROM N.A. TISSUS-GILL | MEDLINE-9017, | MEDLINE-94255438; PubMed=8197156; MEDLINE-94255438; PubMed=8197156; MEDLINE-94255438; PubMed=8197156; MEDLINE-94255438; PubMed=8197156; Martine-97, Martine-97, Milhaud G., Benson A.A., Moukhtar M.S., Cressent M.; The calcitonin gene is expressed in salmon gills."; Proc. Natl. Acad. Sci. U.S.A. 91:4912-4914(1994). EMBL: X78080; CAA54988.1; EMBL: X78080; CAA54988.1; EMBL: X78080; CAA54988.1; Proc. PRO01093; Calcitonin-like. InterPro: PRO01093; Calcitonin-like. InterPro: PRO01395; Calcitonin-like. PRON135; PRO0130; CALCITONINA. SWART; SMO0131; CALCITONINA. SWART; PRO0258; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 34 CALCITONIN.
56 AA; 6165 MW; B073F85C56C1848F CRC64;
                                                                   01-NoV-1996 (TrEMBLrel. 01, Created)
01-NoV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
calcitonin (Fragment).
                                    56 AA.
                                    PRT;
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Best Local Similarity 100.0
Matches 33; Conservative
                                    PRELIMINARY;
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2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34

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091970; 091970

RESULT 2 091970

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SEQUENCE FROM N.A. Zhang G.G., Yang G.P., Zhang X.C.; Zhang B.H., Mac Y.X., Wang G.G., Yang G.P., Zhang and Sequence Analysis of Salmon Calcitonin Genes from Three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGUENCE FROM N.A.
Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
"Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three Different Sources.";
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF491872; AAL99993.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TaxID=190488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryyii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TAXID-8017;
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                                                                                                                      Length 62;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AR491874; AAL99995.1; -.
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                                                                                 62 AA; 6865 MW; EE8AA50D5ED4CA99 CRC64;
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                    97.3%; Score 178; DB 13;
100.0%; Pred. No. 3.3e-20;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                              9 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 41
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PRINTS; PR00270; CALCITONINA.
SMART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                               Query Match
Best Local Similarity 100.
Matches 33; Conservative
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Matches 32; Conserv
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Q8QG82;
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Q8QG84
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                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calcitonin I (Fragment).
0ncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
0ncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
Netriopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95047488; PubMed=7959002;
MEDLINE=95047488; PubMed=7959002;
Martial K., Maubras L., Taboulet J., Jullienne A., Milhaud G.,
Moukhtar M.S., Cressent M.;
"Production of salmon calcitonin I in Oncorhynchus gorbuscha by
alternative polyadenylation of two RNA species.";
Gene 149:277-281(1994).
EMBL: S74353; AAD14152.1; -.
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Jansz H.S., Zandberg J.;
"Identification and partial characterization of the salmon calcitonin/CGRP gene by polymerase chain reaction.";
Ann. N. Y. Acad. Sci., 657:63-69(1992).
EMBL; 804096; AAB22592.1;
HSSP; P01262; IBKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 59;
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Last annotation update)
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Pred. No. 3.1e-20;
Mismatches 0;
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          CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 35
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InterPro; IPR001935; Calcitonin_A.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
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InterPro; 1PR01693; Calcitonin-like.
InterPro; 1PR001935; Calcitonin_A.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00270; CALCITONINA.
SMART; SW00113; CALCITONIN; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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NON_TER SEQUENCE

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygli; Neopterygli: Teleostei; Euteleostei;
Protacanthopterygli: Salmoniformes; Salmonidae; Salvelinus.
NCBL_TaxID=8036;
                                                                                                                                                                                                      Oncorhynchus kisutch (Coho salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TaxID=8019;
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SEQUENCE FROM N.A.
Zhang B., Mao Y., Wang G., Zhang X.;
"Cloning and Sequence Analysis of Salmon Calcitonin Genes of
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SEQUENCE FROM N.A.
Zhang B., Mao Y., Wang G., Zhang X.;
"Cloning and Sequence Analysis of Salmon Calcitonin Genes
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EmBL; AF497758; AAM18089.1; -.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF497757; AAM18088.1; -.
NON_TER 1 1
NON_TER 32 32
SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;
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                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
calcitonin (Fragment).
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Last annotation update)
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100.0%; Pred. No. 1.3e-19;
tive 0; Mismatches 0;
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Local Similarity 100.0%; Pred. No. 1.3e-19;
hes 32; Conservative 0; Mismatches 0;
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last and
Calcitonin (Fragment).
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Best Local Similarity 100.0
Matches 32; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostel; Euteleostel; Protacanthopterygli; Salmoniformes; Salmonidae; Salmo.
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SEQUENCE FROM N.A.
Zhang B., Mao Y., Wang G., Zhang X.;
"Cloning and Sequence Analysis of Salmon Calcitonin Genes of
                                                                                                                                                                                                                                                                                                                                                                                Zhang B., Mao Y., Wang G., Zhang X.;
*Loloning and Sequence Analysis of Salmon Calcitonin Genes of
Anacoulture.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 94.0%; Score 172; DB 13; Length 32; Local Similarity 100.0%; Pred. No. 1.3e-19; es 32; Conservative 0; Mismatches 0; Indels
              Query Match
94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AF497756; AAM18087.1; '...
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF497755; AAM18086.1;
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32 AA; 3435 MW; AFC935519807E7C2 CRC64;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Calcitonin (Fragment).
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Matches 32; Conservative
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Matches
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                   Calcitonin,
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P79813;
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HSSP;
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Matches
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P79813
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
Zhang and Sequence Analysis of Salmon Calcitonin Genes from Three Different Sources.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF491873; AAL99994.1;
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha: Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                         Oncorhynchus keta (Chum salmon).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei;
Protacanthopterygli; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8018;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ309015; CAC81278.1; - CALCITONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 136 AA; 14997 MW; A9A9FA80D3E584E4 CRC64;
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                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Pred. No. 6.1e-18;
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                                        32 AA
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Calcitonin.
                                                                             (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
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                                        PRELIMINARY;
                                                                                                                                       Calcitonin (Fragment).
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                                                                                              01-JUN-2002
01-JUN-2002
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SEQUENCE
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                                                                                                                                         MEDLINE=93202415; PubMed=8454163; Sasayama Y., Watanabe T.X., Sasayama Y., Ukawa K., Kai-Ya H., Oguro C., Takei Y., Watanabe T.X., Nakajima K., Sakakibara S.; Roldiish K., Sakakibara S.; Ooldiish calcitonin: purification, characterization, and hypocalcemic potency.";
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Carassius auratus (Goldfish).
Ebkaryota: Metazoa: Chordata: Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-9705724; Pubmed-8901583; Mansz H., Martial K., Zandberg J., Milhaud G., Benson A.A., Julianne A., Moukhtar M.S., Cressent M.; "Identification of a new calcitonin gene in the salmon Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcitonin 4 (Fragment).

Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8017;
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CARBOXY TERMINAL PEPTIDE.
1316EEB8EBACF199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00258; CALCITONIN; 1.
SEQUENCE 32 AA; 3390 MW; AFC93549F818560F CRC64;
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Last annotation update)
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EMBL, U71286; AAB38532.1; -.
HSSP; P01262; 1BKU.
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Pred. No. 4.4e-17;
4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                            HSSP; P01262; 1BKU;
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR0016935; Calcitonin.A.
Pfam; PF00214; Calc_CGRP_IARP; I.
PRINTS; PR00270; CALCITONIN.
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InterPro; IPR001935; Calcitonin_A.
Pfam; PF00214; Calc_CGRP_IAPP; I.
PRINTS; PR00270; CALCITONINA.
SMARY; SM00113; CALCITONIN; I.
PROSITE; PS00258; CALCITONIN; 1.
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01-MAY-1997 (TrEMBLrel. 03, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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90.6%;
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6860 MW;
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84.8%;
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Best Local Similarity
Matches 28; Conserv
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es 29; Conserv
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62 AA;
                                                                        Cyprinidae; Cara
NCBI_TaxID=7957;
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MEDLINE-21406117; PubMed-11514025;
Suzuki N., Suzuki T., Kurokawa T.;
MENA expression in flounder, Paralichthys olivaceus.";
Peptides 22:1435-1438(2001).
PEMBL, AB052782; BAB64410.1; -
Interpro; IPR001693; Calcitonin-like.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 20, Last annotation update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
03-Lius qallus (Chicken).
04-Lius (Chicken).
05-Lius (Chicken).
05-Lius (Chicken).
06-Lius (Chicken).
06-Lius (Chicken).
06-Lius (Chicken).
06-Lius (Chicken).
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T FEBS Lett. 223:63-68(1987).

R EmbL; X05313; GA326432.1; -.

R EmbL; X05313; GA326432.1; -.

R InterPro: IPR001693; Calcitonin-like.

R InterPro: IPR001895; Calcitonin-like.

R Pfan: PF00214; Calc.CGPP. IAPP; 1.

R PRINTS; PR00270; CALCITONINA.

R SMRAT; SM00113; CALCITONINA.

R PROSITE; PS002269; CALCITONINA.

R PROSITE; PS002269; CALCITONINA.

R PROSITE; PS002269; CALCITONINA.

R SEQUENCE 65 AA; 7232 MW; 772C54DA8A5ABCOB CRC64;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei;
Acanthomorpha, Acanthopterygli; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.8%; Score 157; DB 13; Length 65; Best Local Similarity 84.8%; Pred. No. 6.7e-17; Matches 28; Conservative 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 CALCITONIN.
5426 MW; ABDB859A27DA249F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calcitonin (Fragment).
CT/CGRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CASLSTCVLGKLSQELHKLQTYPRTDVGAGTPG 41
2 CSNLSTCVLGKLSQELHKLQTYPRINTGSGTPG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AA
                                                                                                                                                          65 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=8803046; PubMed=3666142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q90YC4
Q90YC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                       Q9W6Z3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                        RESULT 14
                                                                                                                                Q9W623
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Gaps
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Pred. No. 7.1e-17;
4; Mismatches 2; Indels
                              Best Local Similarity 81.8%;
Matches 27; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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May 30, 2003, 09:49:44; Search time 14 Seconds (without alignments) 71.456 Million cell updates/sec
OM protein - protein search, using sw model
                                                    Run on:
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183 1 mcsnlstcvlgklsqelhklqtyprtntgsgtpg 34 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/iaa/5A_COMB.ppp:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.ppp:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.ppp:*
// /cgn2_6/ptodata/1/iaa/6B_COMB.ppp:*
5: /cgn2_6/ptodata/1/iaa/PtorUS_COMB.ppp:*
6: /cgn2_6/ptodata/1/iaa/PtorUS_COMB.ppp:* Issued_Patents_AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

														•															
	Description	Sequence 7. Appli	ò	9	7,	4,	7	4	9	H	31,	43,	38,	2, 2	5,		38,	Sequence 2, Appli	'n	4	Patent No. 5183802	Sequence 8, Appli	4	20,	20,	ď,	Sequence 3, Appli	1,	
	ID	US-07-776-272-7	-07-952	-164	US-08-164-408A-7	US-07-794-288D-4	US-08-176-153-2	-08-424	-477	-08-477-7	-477	US-08-477-727A-43		US-08-847-007A-2	US-09-071-090-2	US-09-139-819A-38	US-09-750-913-38	•	PCT-US94-14303-2	PCT-US96-05372-4	5183802-3	US-07-776-272-8	US-08-907-602-1	US-08-467-472C-20	-60	0	9	US-08-424-866-1	
	Match Length DB	33 1	32 1		32 1		32 1	32 1					32 2		32 3	32 4	32 4		32 5					~	~	32 1	7	32 1	
* Ouerv	Match I	97.3	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0		94.0	94.0					94.0		94.0	94.0		89.1				86.9		
	Score	178	172	172	172	172	172	172	172	172	172	172	172	172	172	172	172	172	172	172	172	165	163	162	162	159	159	159	
Result	No.	a	,7	e	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

Sequence 2, Appli Sequence 37, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 37, Appl Sequence 37, Appl Sequence 1, Appli Patent No. 5183802 Sequence 21, Appl	39,	Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 40, Appl Sequence 45, Appl
US-08-322-386B-2 US-08-595-868C-37 US-08-847-007A-3 US-09-071-090-3	US-09-750-913-37 US-09-750-913-37 PCT-US96-05372-1 5183802-4 US-08-467-472C-21	US-09-384-061-21 US-08-595-868C-39 US-09-139-819A-39 US-09-750-913-39	US-08-847-007A-7 US-08-847-007A-7 US-09-071-090-7 US-08-595-868C-40 US-07-401-432-45
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159 159 159 159	10000 10000 10000 10000	158	155 155 154
3355 330 310 310	7 W W W W 1 W 4 12 0	7 8 8 8 4 4 7 8 8 9 0 +	14444 19645

ALIGNMENTS

RESULT 1

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Sequence 7, Application US/07776272
Patent No. 5612454
GENERAL INFORMATION:
APPLICANT: Kaninuma, Toshihiko
APPLICANT: Tajima, Masahiro
TITLE OF INVENTION: Process for Purification of Polypeptide
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.3%; Score 178; DB 1; Length 33; Best Local Similarity 100.0%; Pred. No. 2.4e-17; Matches 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ASALING LON
COUTRY:
COUNTRY:
CONTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 440706
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 33 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTPG 34

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                                                                            GENERAL INFORMATION:
APPLICANT: TAKAHASHI, Yoshio
APPLICANT: TAKAHASHI, AVIOShi
APPLICANT: TAKAHASHI, AVIOShi
APPLICANT: TAKIGAMA, Wasaharu
APPLICANT: TAKIGAWA, Wasaharu
TITLE OF INVENTION: NOVEL CALCITONIN AND METHOD FOR THE
TITLE OF INVENTION: PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                           AUDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marcos C
Berta P.
Gemma J.
Procedure for Preparing Salmon
Calcitonin
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,735A
FILING DATE: 30-NOV-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.0%; Score 172; DB 1; I 100.0%; Pred. No. 1.5e-16; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROCE APPLICATION DATA:
APPLICATION NUMBER: JP 129695/1991
FILING DATE: 31-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 249322/1991
FILING DATE: 27-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 011900-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-6620
TELEFAX: (703)836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08164408A
Patent No. 5527881
GENERAL INFORMATION:
APPLICANT: Poblet, Marcos C
APPLICANT: Obiols, Berta P.
APPLICANT: Farres, Genma J.
TITLE OF INVENTION: Procedure for P
TITLE OF INVENTION: Calcitonin
  RESULM 4
US-07-952-735A-6
; Sequence 6, Application US/07952735A
· Patent No. 5440012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-07-952-735A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-164-408A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Poblet, Marcos C
APPLICANT: Obiols, Berta P.
APPLICANT: Farres, Genma J.
TITLE OF INVENTION: Procedure for Preparing Salmon TITLE OF INVENTION: Calcitonin
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 94.0%; Score 172; DB 1; L
Local Similarity 100.0%; Pred. No. 1.5e-16;
nes 32; Conservative 0; Mismatches 0;
               CORRESPONDENCE ADDRESS:
ADDRESSEE. Wigman, Cohen, Leitner, & Myers, F
STREET: 1735 Jefferson Davis Hwy., Suite 200
CITY: Allington
                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, Kb storage
COMPUTER: IQ 486
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                  UNBER: US/08/164,408A
                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,408A
FILING DATE: 09-DEC-1993
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REBERNENCE/DOCKET NUMBER: 3721-A
TELECHONE: (703)413-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with tert-buty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7, Application US/08164408A; Patent No. 5527881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)413-8129
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION OTHER INFORMATION
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                                                                               Virginia
: USA
                                                                               STATE: Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-164-408A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-164-408A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Center
633 West Fifth Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 32 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
                                     Suite 4700
                                                         Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: US-07-794-288D-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                   COUNTRY: U.S.A. ZIP: 90071-2066
                                                              CITY: L
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Threat position 7 substituted with tert-butyl cys at position 7 substituted with trityl by at position 11 substituted with trityl ser at position 13 substituted with trityl solution 13 substituted with tert-butyl dlu at position 15 substituted with tert-butyl lys at position 17 substituted with trityl Lys at position 18 substituted with trityl Thr at position 21 substituted with trityl Try at position 22 substituted with tert-butyl Arg at position 24 substituted with tert-butyl Arg at position 24 substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arg at position 24 substituted with 2,2,5,7,8-pentamethylcroman-6-sulphonyl Thr at position 25 substituted with tert-butyl Far at position 27 substituted with tert-butyl Ser at position 29 substituted with tert-butyl Thr at position 31 substituted with tert-butyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ser at position 5 substituted
ADDRESSEE: Wigman, Cohen, Leitner, & Myers, P.C. STREET: 1735 Jefferson Davis Hwy., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 172; DB 1; 1
Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOWARD JONES,
APPLICANT: LAURA S.L. GAETA,
APPLICANT: KATHRYN S. PRICKETT and
APPLICANT: KEVIN BEAUMONT
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, Kb storage COMPUTER: IQ 486
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.0%; Scor. 100.0%; Pred. No. 1. 0. Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,408A
FILING DATE: 09-DEC-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REFERNE/DECAFET NUMBER: 37,21-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07794288D Patent No. 5580953 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFA: (703)413-8129
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FEATURE:
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OTHER INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
                                     Arlington
                                                                Virginia
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US-07-794-288D-4
                                     CITY: Ar
STATE: V
COUNTRY:
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Length 32;
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APPLICATION NUMBER: US/08/176,153
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.0%; Score 172; DB 1; I Best Local Similarity 100.0%; Pred. No. 1.5e-16; Matches 32; Conservative 0; Mismatches 0;
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: Mb storage
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATE: WordPerfect (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,288D
FILING DATE: Herewith
CLASSIFICATION: 5.14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/794,288
FILING DATE: 19.00-91
RILING DATE: 19.00-91
RILING DATE: 19.00-91
REGISTRATION: NUMBER: 32.219
REFERENCE/DOCKET NUMBER: 193/153
TELECOMMUNICATION NUMBER: 193/153
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US-08-176-153-2
Sequence 2, Application US/08176153
Sequence 2, Application US/08176153
SPAPLICANT: Labroo, Virender
APPLICANT: Labroo, Virender
SPAPLICANT: Sasaki, Tomikazu
TITLE OF INVENTION: DERIVATIZED CALCITONINS
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Pred. No. 1.5e-16;
100.0%; Pred. No. 1.5e-16; attive 0; Mismatches 0;
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                                                          2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                 1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                                                             Sequence 6, Application US/0847727A
Sequence 6, Application US/0847727A
Septent No. 5739106
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Young, Andrew
APPLICANT: Pecley, Nigel
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: APPETITE REGULATING
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFFWARE: FESTSEM OFFSION 1.5
CURRENT APPLICATION NUMBER: US/08/477,727A
FILING DATE: 0'--JUN-1995
CLASSIPICATION 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08477727A
Patent No. 5739106
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Best Local Similarity 100.0%; P.
Matches 32; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
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NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
  Best Local Similarity 100.0
Matches 32; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 633 WEST I CITY: LOS ANGELES STATE: CA
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NO. 57212071e, John F.
APPLICANT: Abajian, Henry B.
TITLE OF INVENTION: Method of Treatment of Pain
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               94.0%; Score 172; DB 1; 100.0%; Pred. No. 1.5e-16; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.0%; Score 172;
    ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENGE/DOCKET NUMBER: 92-20C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 427
TELEPACK: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 5370 Manhattan Circle, Sui
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33878
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
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                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 32; Conservative
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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FILING DATE: 18-APR
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TELEFAX: (
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Pred. No. 1.5e-16;
0; Mismatches 0;
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100.0%; Pred. No. ...
... 0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEB: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/0847727A
Patent No. 5739106
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Young, Andrew
APPLICANT: Percekt, Nigel
APPLICANT: Beeley, Nigel
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                             OCTAIN. AND CONTROLL OF CONTROL O
   STAIL:
COUNTY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"TWOTTER: IBM COMPALIBLE
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.1
Matches 32; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.0%; Score 172; DB 1; I 100.0%; Pred. No. 1.5e-16; tive 0; Mismatches 0;
                                 APPLICANT: Young, Andrew
APPLICANT: Beeley, Nigel
APPLICANT: Beeley, Nigel
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/0847727A
Patent No. 5739106
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Rong, Andrew
APPLICANT: Paceley, Nigel
APPLICANT: Prickett, Rathryn
TITLE OF INVENTION: CAMPOSITIONS
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESTESD VEFSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
RECISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Conservative
                           Rink, Timothy
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: SORIGINAL SOURCE: US-08-477-727A-18
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-477-727A-31
                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                          STATE:
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Gaps

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NAME/KEY: Modified-site
LOCATION: 1..7
OTHER INFORMATION: /label= Disulfide bond
OTHER INFORMATION: /note= "A disulfide bond exists between the
OTHER INFORMATION: /note= "A disulfide bond exists between the
OTHER INFORMATION: two sulfur atoms of the cysteine residues;
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O
                                                                                                                                                                                                                                                                         Length 32;
                                                                                                                                                                                                                                                                                                                      Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,007A
FILING DATE: U1 MAY-1997
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: NO. 6083480nan, Kevin E
REGISTRATION NUMBER: 35,303
REERENOCAPOCKET NUMBER: 35,303
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                           Score 172; DB 2; I
Pred. No. 1.5e-16;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: MCDONNEL & Bergho STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                        1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                                                                                                                                                                                                                                 2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Bush, Larry R
APPLICANT: Pearson, Daniel P
APPLICANT: Lister-James, John
IITLE OF INVENTION: Radiolabeled Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
LOCATION: 32
OTHER INFORMATION: /label= Amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08847007A Patent No. 6083480
                                                                                                                                                                                                                                                                             Ouery Match 94.0%; Scc
Best Local Similarity 100.0%; P1
Matches 32; Conservative 0;
                                                                                                                                                                                                N-terminal
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                                             32 amino acids
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TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                      single
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                                                             TYPE: amino acid
STRANDEDNESS: si
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STREET: 300
TTV; Chicago
                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: N-ORIGINAL SOURCE: US-08-595-868C-38
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APPLICANT: Stout, Jay
APPLICANT: Stout, Jay
APPLICANT: Henriksen, Dennis
APPLICANT: Holmquist, Bart
APPLICANT: Frank, Julie
TITLE OF INVENTION: RECOMBINANT PREPARATION OF CALCITONIN FRAGMENTS AND US
CORRESPONDENCE ADDRESS:
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STREET: 3100 No. 5962270west Center, 90 S. 7th Street
CITY: Minneapolis
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94.0%; Score 172; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,868C
FILING DATE: 06-FEB-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 8648.59US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-595-868C-38
; Sequence 38, Application US/08595868C
; Patent No. 5962270
                                                                                          NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REPERENCE/DOCKET NUMBER: 214/(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal ORIGINAL SOURCE:
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         PRIOR APPLICATION DATA: APPLICATION NUMBER:
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APPLICANT: Wagner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                      FILING DATE:
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COUNTRY:
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CITY: Washington STATE: D.C.
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/note≈ "The carboxyl terminus is modified to an amide"
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                                                                                                                                                                                                      Sequence 2, Application US/09071090

Sequence 2, Application US/09071090

Setent No. 6086850

GENERAL INCRMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Pearson, Daniel A.
APPLICANT: Lister-James, John
TITLE OF INVENTION: CALCITONIN RECEPTOR BINDING REAGENTS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: Deatide, Inc.
STREET: Londonderry
COLTY: Londonderry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                94.0%; Score 172; DB 3; Length 32; 100.0%; Pred. No. 1.5e-16; 1.ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/071,090
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.0%; Score 172; DB 3; I
100.0%; Pred. No. 1.5e-16;
Live 0; Mismatches 0;
                                                                                                                                                                               1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
                                                                                                                                                         2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /product= "PROLINE 32"
OTHER INFORMATION: /label= amide
US-09-071-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MCDENIELS, PATILOIS A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 125.1PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/847,007
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: both
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: CALCITONIN--SALMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
                                                                                Query Match 94.03
Best Local Similarity 100.(
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 32; Conservative
     ) OTHER INFORMATION:
; OTHER INFORMATION:
US-08-847-007A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                 RESULT 14
US-09-071-090-2
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FRAGMENTS AND USE THEREOF IN THE PREPARATION OF CALCITONIN AND RELATED ANALOGS 51
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                                                                                                                                                                                                                                                     APPLICANT: STOUT, JAYS.
APPLICANT: HENRIKSEN, Dennis B.
APPLICANT: HENRIKSEN, Dennis B.
APPLICANT: PARTRIDGE, Buruce E.
APPLICANT: HOLMOUIST, Bart
APPLICANT: FRANK, Julie A.
TITLE OF INVENTION: RECOMBINANT PREPARATION OF CALCITONIN TITLE OF INVENTION: FRAGMENTS AND USE THEREOF IN THE PREPARATION: OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPALILLA OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/09/139,819A APPLICATION NUMBER: US/09/139,819A FILING DATE: 25-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.0%; Score 172; DB 4; I
100.0%; Pred. No. 1.5e-16;
Live 0; Mismatches 0;
                        1 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 32
2 CSNLSTCVLGKLSQELHKLQTYPRTNTGSGTP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PHIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/595,868
FILING DATE: 06-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTREAME,DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 089187/0144
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 30, 2003, 09:51:38
Job time : 15 secs
                                                                                                                                                         Sequence 38, Application US/09139819A; Patent No. 6251635; GENERAL INFORMATION: APPLICANT: WAGNER, Fred W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 672-530
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 3
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Best Local Similarity 100.0
Matches 32; Conservative
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MOLECULE TYPE: peptide
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